Attorney Docket No. 02-106720US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:	
Juha Punnonen, et al.	Examiner: Unassigned
Application No.: 09/888,324	Art Unit: 1643
Filed: June 22, 2001	LETTER TO OFFICIAL DRAFTSPERSON
For: NOVEL CO-STIMULATORY MOLECULES	

Attn:
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Applicant hereby submits 39 sheets of formal drawings to be made of record in the above-identified case.

Respectfully submitted,

Emily M. Haliday, J.D., Ph.D.
Reg. No. 38,903

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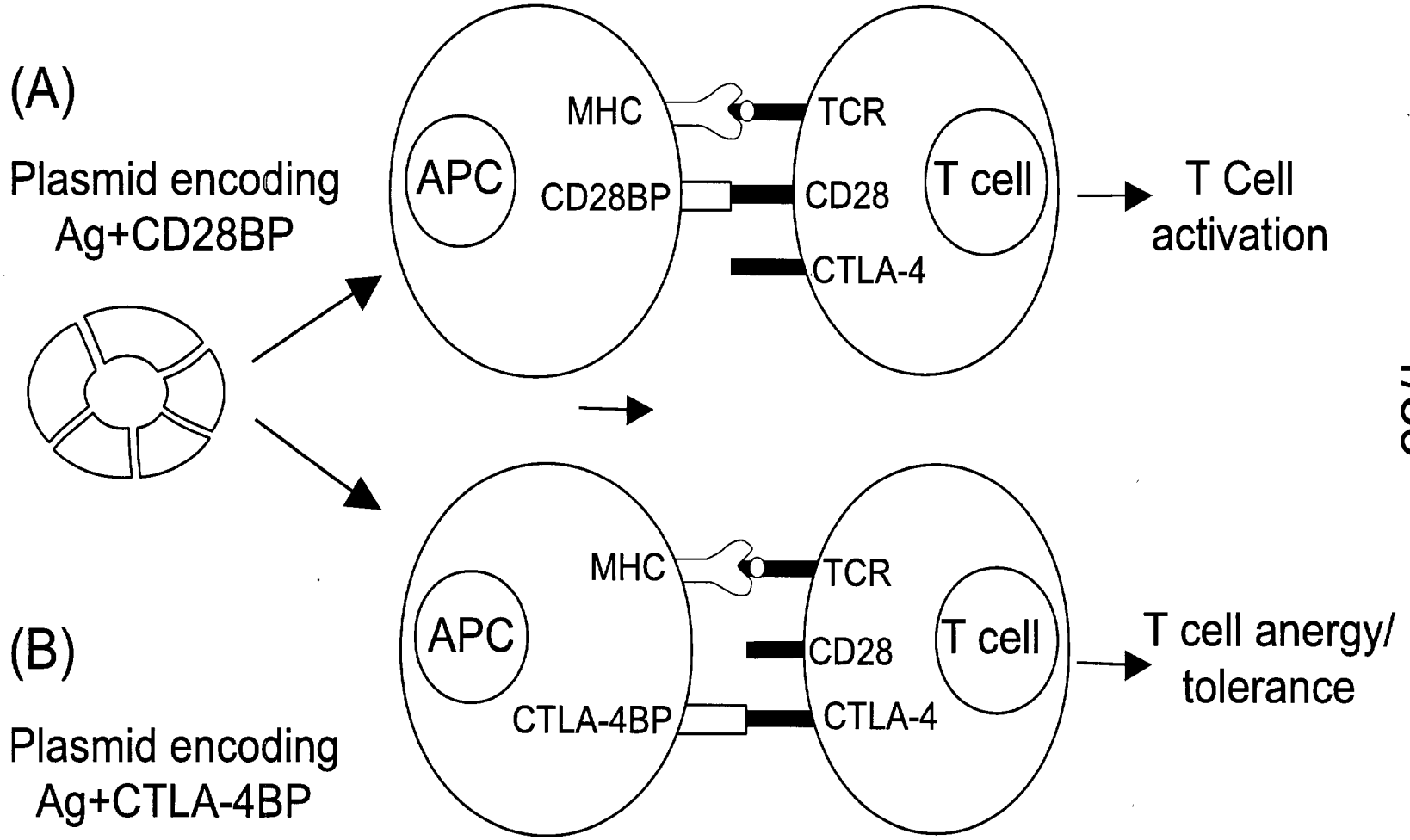
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Fig. 1

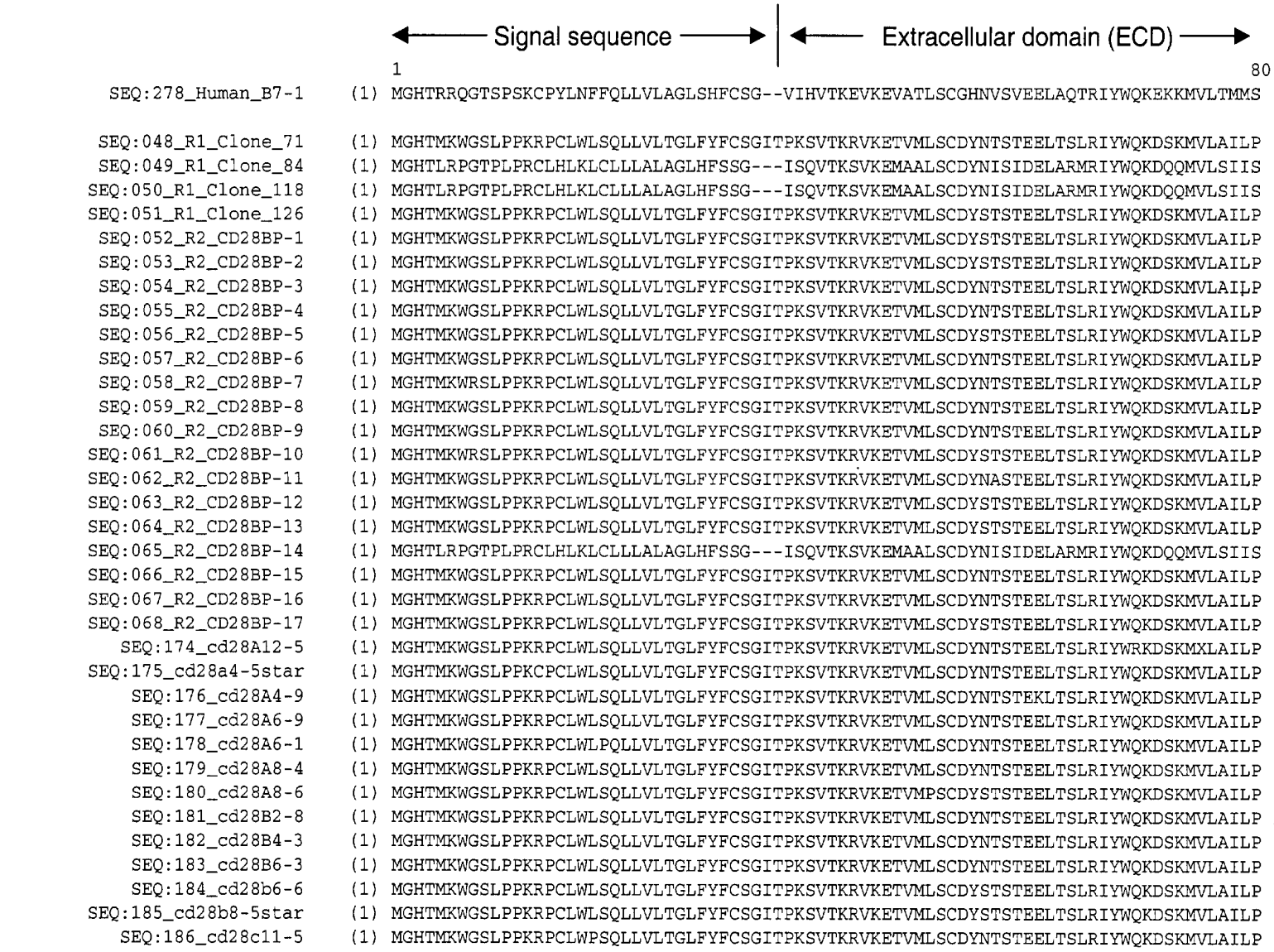
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Fig. 2A

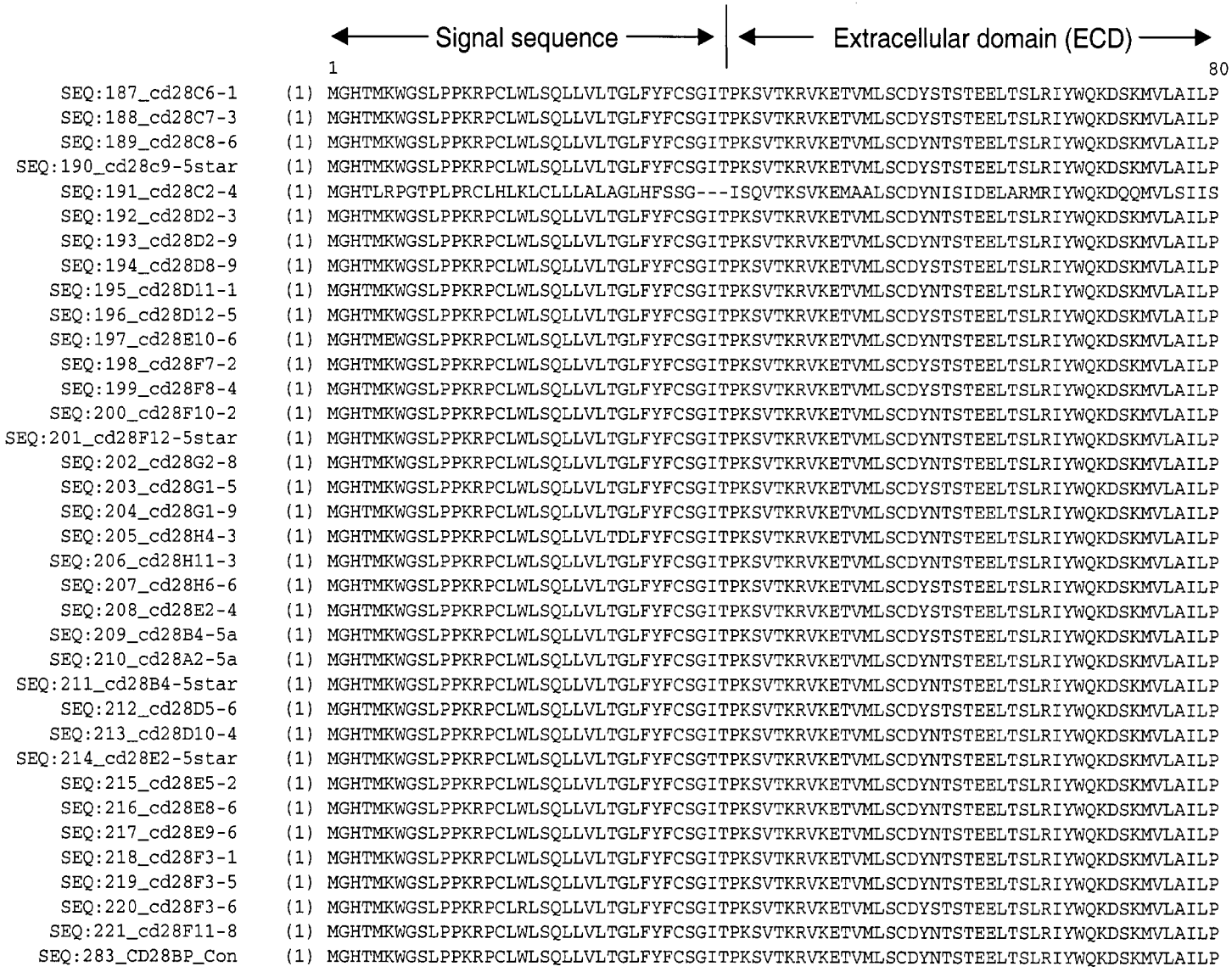
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Fig. 2B

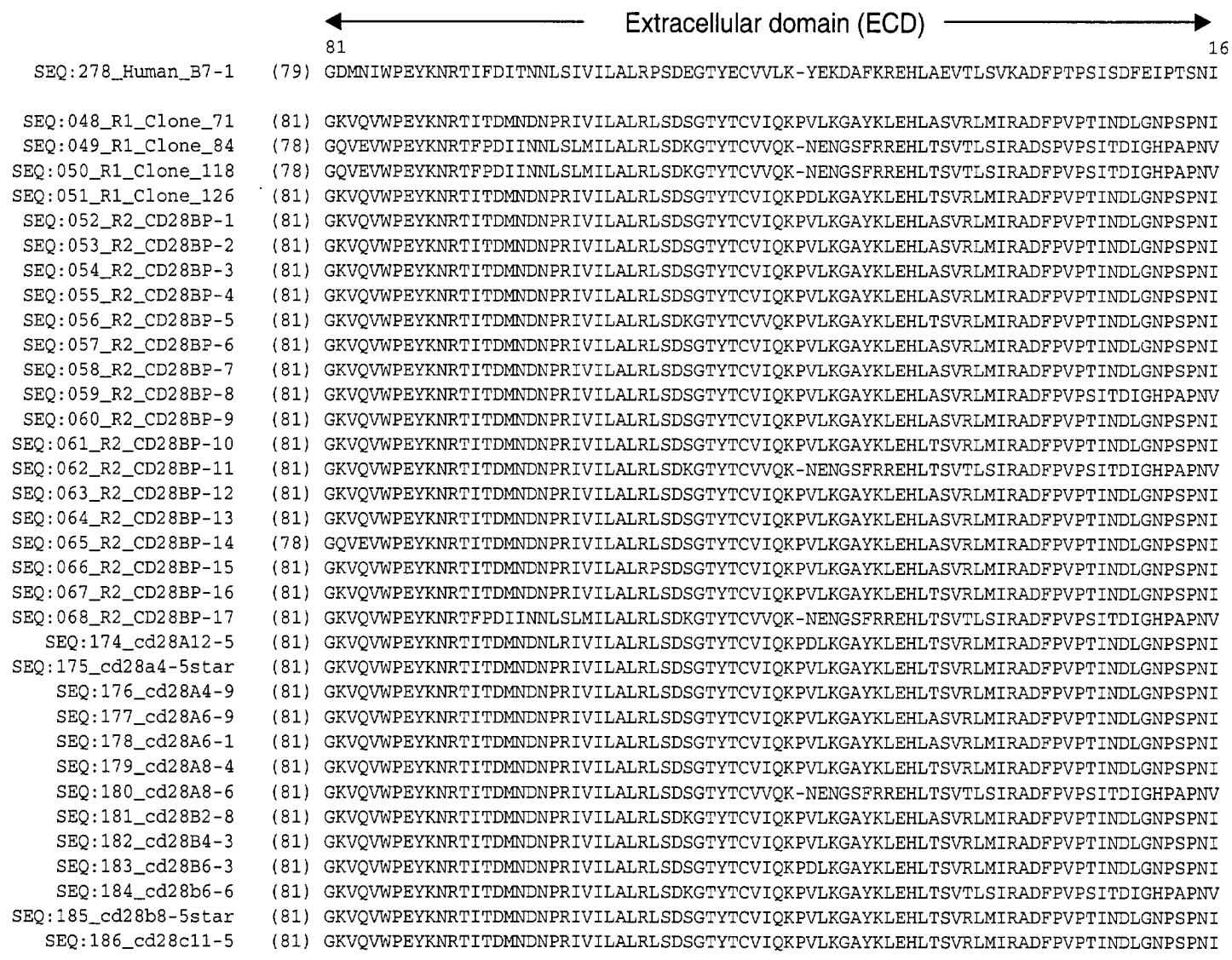
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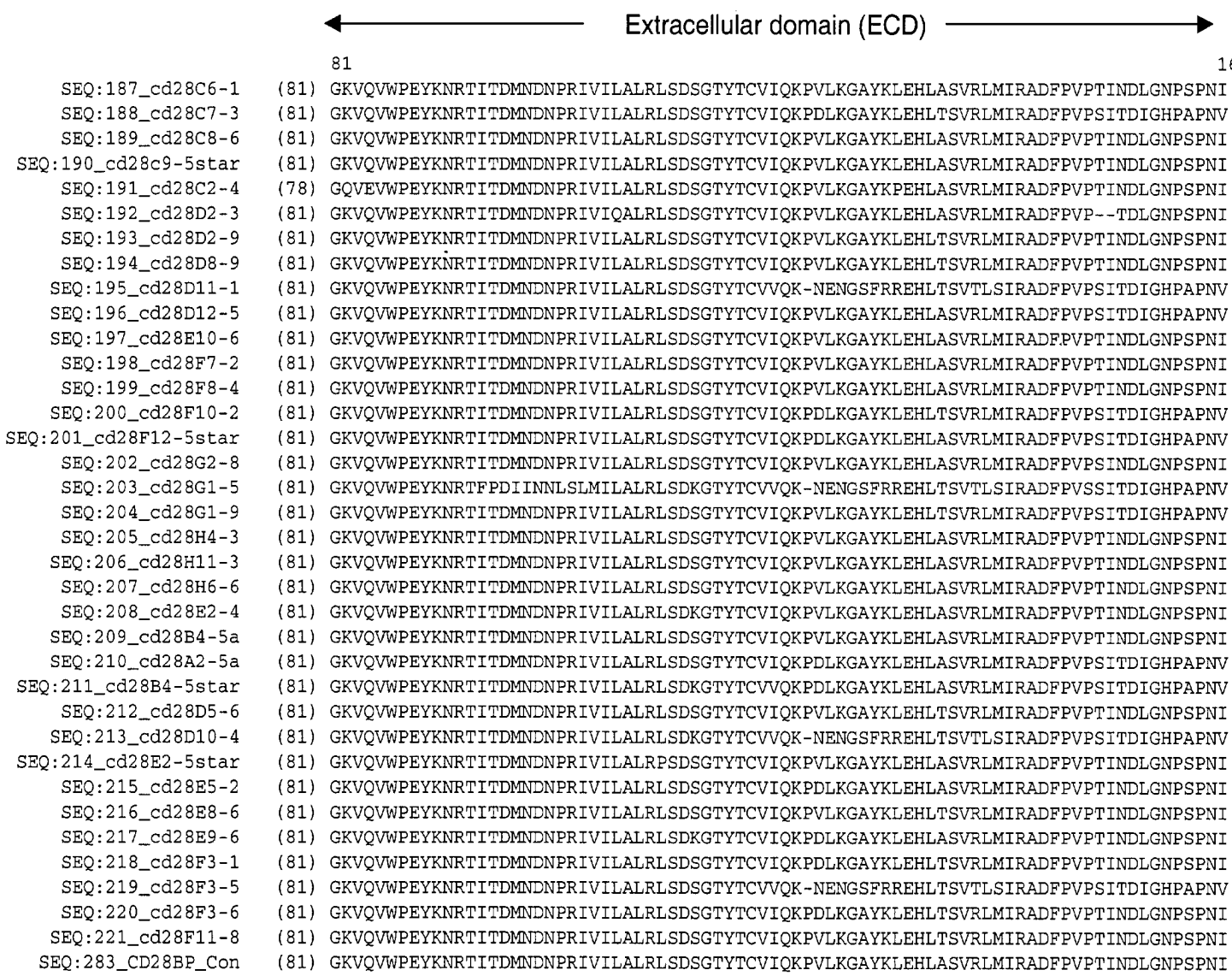
Fig. 2C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SEQ:196_cd28D12-5 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPSITDIGHPAPNV
SEQ:197_cd28E10-6 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
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SEQ:202_cd28G2-8 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPSINDLGNPSPNI
SEQ:203_cd28G1-5 (81) GKVQVWPEYKNRTFPDIINNLSLMILALRLSDKGTYTCVVQK-NENGSFRREHLTSVTLSIRADFPVSSITDIGHPAPNV
SEQ:204_cd28G1-9 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLTSVRLMIRADFPVPSITDIGHPAPNV
SEQ:205_cd28H4-3 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
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SEQ:214_cd28E2-5star (81) GKVQVWPEYKNRTITDMNDNPRIVILALRPSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:215_cd28E5-2 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPDLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
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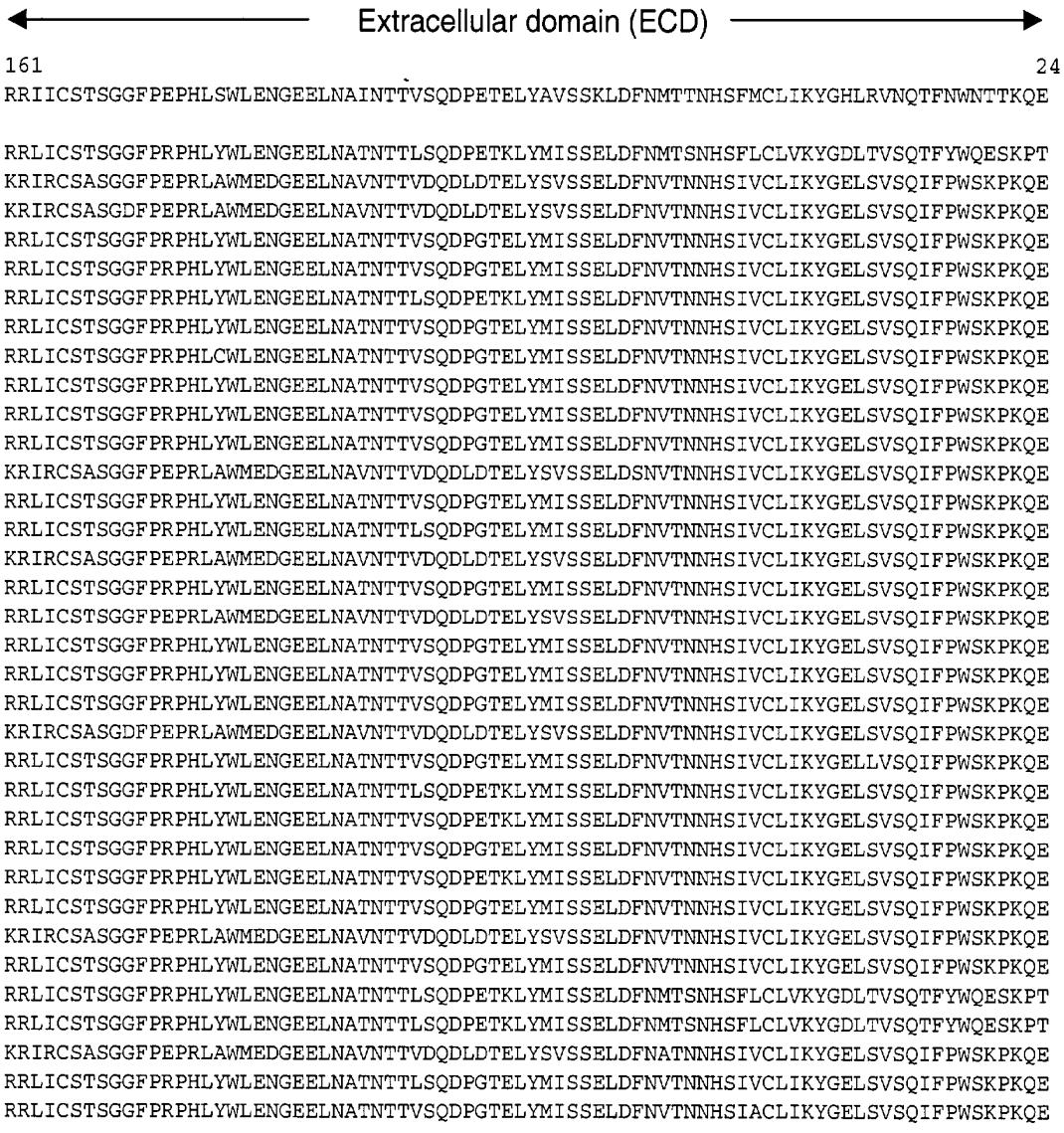
SEQ:283_CD28BP_Con (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI

Fig. 2D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SEQ:058_R2_CD28BP-7 (161) RRLICSTSGGFPRPHLYWLENGEELNATNTTVSQDPGTELYMISSELDFNVTNNHSIVCLIKYGELSVSQIFPWSKPKQE
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Fig. 2E

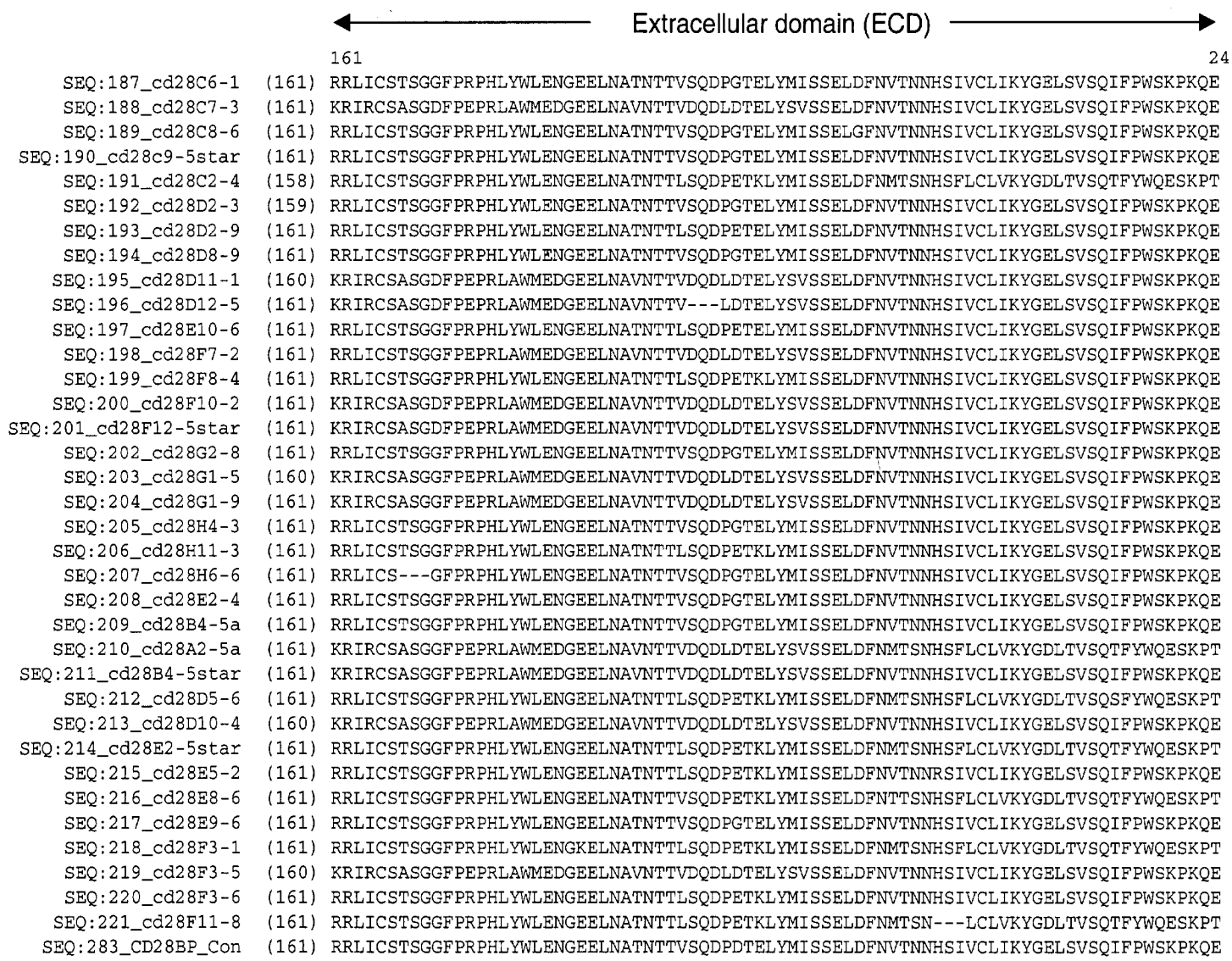
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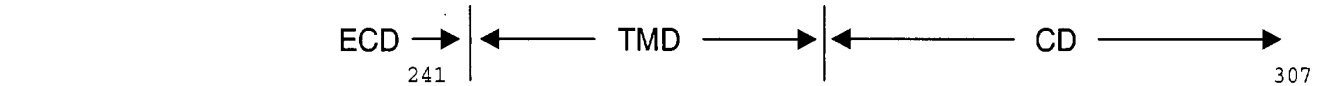
Fig. 2F

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SEQ:064_R2_CD28BP-13 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
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SEQ:066_R2_CD28BP-15 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:067_R2_CD28BP-16 (241) P-PIDQLPFWVIIP---VSGALVLAAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:068_R2_CD28BP-17 (240) P-PIDQLPFWVIIP---VSGALVLTVVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
   SEQ:174_cd28A12-5 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:175_cd28a4-5star (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
    SEQ:176_cd28A4-9 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCPACRHVARWKRTRRNEETVGTERLSPIYLGSAQSRAEVPSLSX
    SEQ:177_cd28A6-9 (241) P-PIDQLPFLVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
    SEQ:178_cd28A6-1 (241) P-PIDQLPFRVIIP---VSGALVLTAIVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
    SEQ:179_cd28A8-4 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
    SEQ:180_cd28A8-6 (240) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
    SEQ:181_cd28B2-8 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
    SEQ:182_cd28B4-3 (241) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVEMQSCSQSP----------
    SEQ:183_cd28B6-3 (241) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVKMQSCSQSP----------
    SEQ:184_cd28b6-6 (241) P-PIDQLPFWVIVP---VSGALVLTAVVLYCLACRHVAR----------------------------
SEQ:185_cd28b8-5star (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
   SEQ:186_cd28c11-5 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
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Fig. 2G

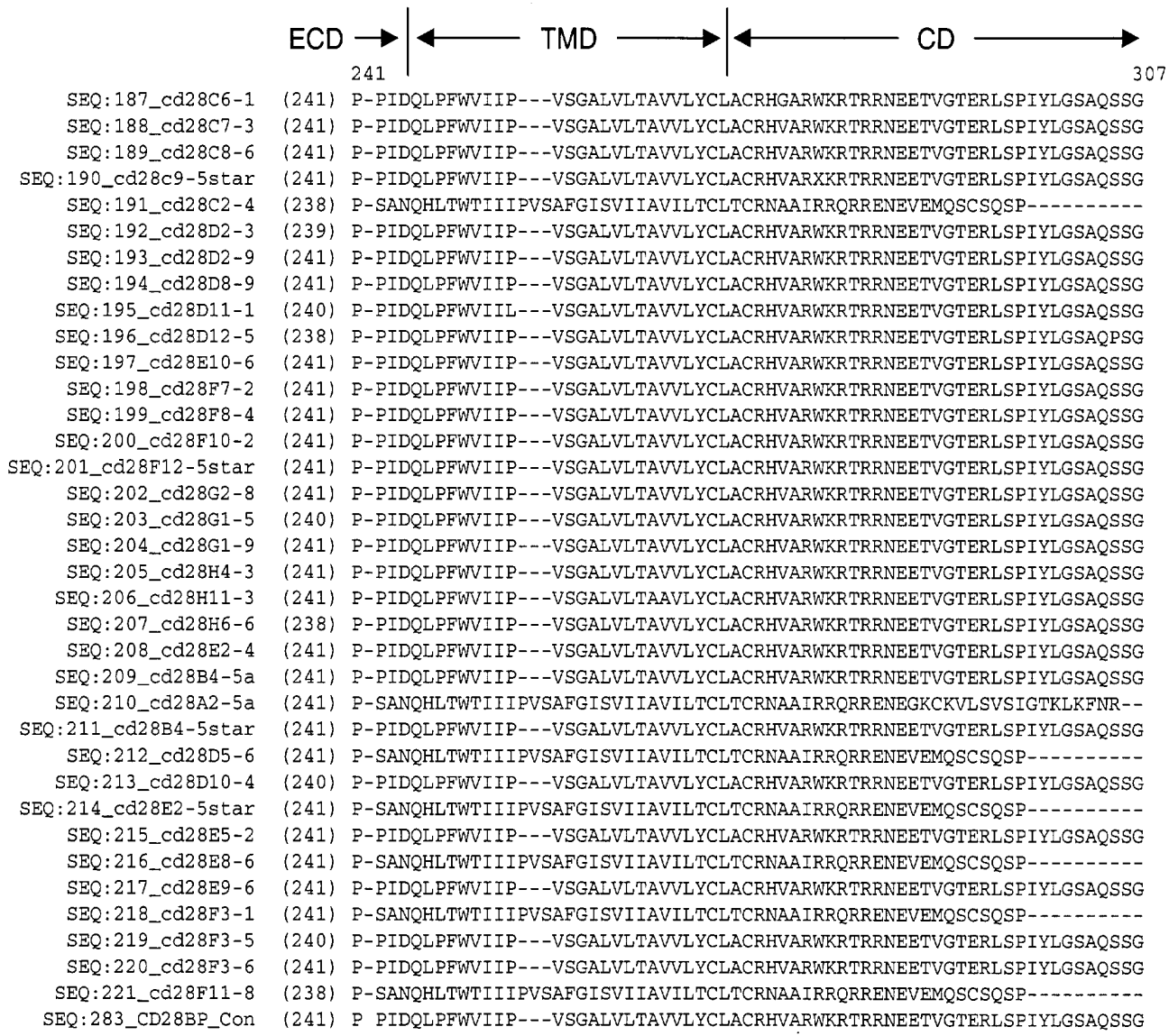
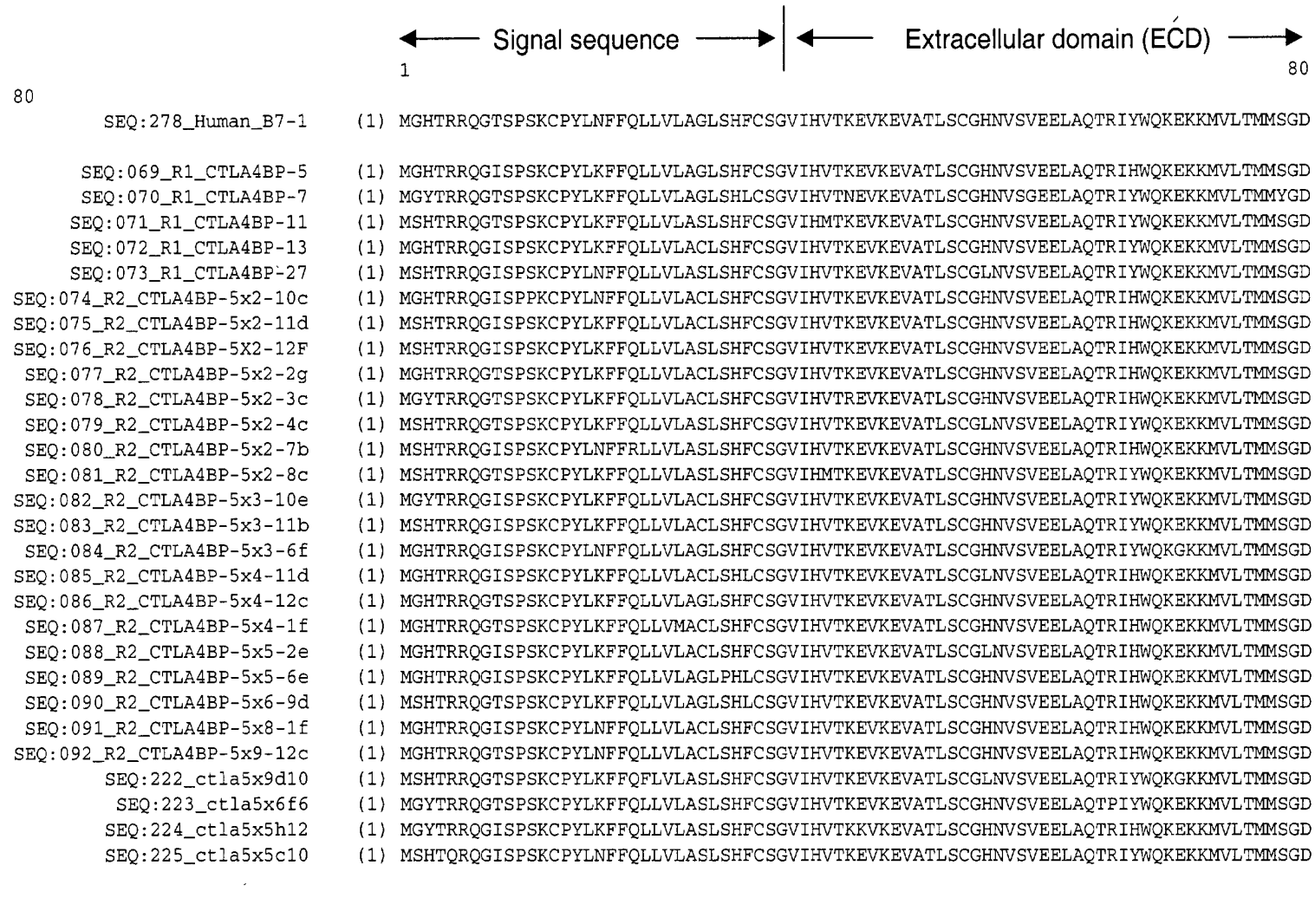

ECD
TMD
CD
241
307
SEQ:187_cd28C6-1 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHGARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:188_cd28C7-3 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:189_cd28C8-6 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:190_cd28c9-5star (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARXKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:191_cd28C2-4 (238) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVEMQSCSQSP----------
SEQ:192_cd28D2-3 (239) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:193_cd28D2-9 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:194_cd28D8-9 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:195_cd28D11-1 (240) P-PIDQLPFWVIIL---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:196_cd28D12-5 (238) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQPSG
SEQ:197_cd28E10-6 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:198_cd28F7-2 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:199_cd28F8-4 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:200_cd28F10-2 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:201_cd28F12-5star (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:202_cd28G2-8 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:203_cd28G1-5 (240) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:204_cd28G1-9 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:205_cd28H4-3 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:206_cd28H11-3 (241) P-PIDQLPFWVIIP---VSGALVLTAAVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:207_cd28H6-6 (238) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:208_cd28E2-4 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:209_cd28B4-5a (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:210_cd28A2-5a (241) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEGKCKVLSVSIGTKLKFNR--
SEQ:211_cd28B4-5star (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:212_cd28D5-6 (241) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVEMQSCSQSP----------
SEQ:213_cd28D10-4 (240) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:214_cd28E2-5star (241) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVEMQSCSQSP----------
SEQ:215_cd28E5-2 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:216_cd28E8-6 (241) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVEMQSCSQSP----------
SEQ:217_cd28E9-6 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:218_cd28F3-1 (241) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVEMQSCSQSP----------
SEQ:219_cd28F3-5 (240) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:220_cd28F3-6 (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:221_cd28F11-8 (238) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVEMQSCSQSP----------
SEQ:283_CD28BP_Con (241) P PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG

Fig. 2H


Signal sequence
Extracellular domain (ECD)
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80
80
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SEQ:069_R1_CTLA4BP-5 (1) MGHTRRQGISPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:070_R1_CTLA4BP-7 (1) MGYTRRQGTSPSKCPYLKFFQLLVLAGLSHLCSGVIHVTNEVKEVATLSCGHNVSGEELAQTRIYWQKEKKMVLTMMYGD
SEQ:071_R1_CTLA4BP-11 (1) MSHTRRQGTSPSKCPYLKFFQLLVLASLSHFCSGVIHMTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:072_R1_CTLA4BP-13 (1) MGHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:073_R1_CTLA4BP-27 (1) MSHTRRQGISPSKCPYLNFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGLNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:074_R2_CTLA4BP-5x2-10c (1) MGHTRRQGISPPKCPYLNFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:075_R2_CTLA4BP-5x2-11d (1) MSHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:076_R2_CTLA4BP-5X2-12F (1) MSHTRRQGISPSKCPYLKFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:077_R2_CTLA4BP-5x2-2g (1) MGHTRRQGTSPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:078_R2_CTLA4BP-5x2-3c (1) MGYTRRQGTSPSKCPYLKFFQLLVLACLSHFCSGVIHVTREVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:079_R2_CTLA4BP-5x2-4c (1) MSHTRRQGTSPSKCPYLKFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGLNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:080_R2_CTLA4BP-5x2-7b (1) MSHTRRQGISPSKCPYLNFFRLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:081_R2_CTLA4BP-5x2-8c (1) MSHTRRQGTSPSKCPYLKFFQLLVLASLSHFCSGVIHMTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:082_R2_CTLA4BP-5x3-10e (1) MGYTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:083_R2_CTLA4BP-5x3-11b (1) MSHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:084_R2_CTLA4BP-5x3-6f (1) MGHTRRQGISPSKCPYLNFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKGKKMVLTMMSGD
SEQ:085_R2_CTLA4BP-5x4-11d (1) MGHTRRQGISPSKCPYLKFFQLLVLACLSHLCSGVIHVTKEVKEVATLSCGLNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:086_R2_CTLA4BP-5x4-12c (1) MGHTRRQGTSPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:087_R2_CTLA4BP-5x4-1f (1) MGHTRRQGTSPSKCPYLKFFQLLVMACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:088_R2_CTLA4BP-5x5-2e (1) MGHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGLNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:089_R2_CTLA4BP-5x5-6e (1) MGHTRRQGISPSKCPYLKFFQLLVLAGLPHLCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:090_R2_CTLA4BP-5x6-9d (1) MSHTRRQGTSPSKCPYLKFFQLLVLAGLSHLCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:091_R2_CTLA4BP-5x8-1f (1) MGHTRRQGISPSKCPYLNFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:092_R2_CTLA4BP-5x9-12c (1) MGHTRRQGTSPSKCPYLNFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:222_ctla5x9d10 (1) MSHTRRQGTSPSKCPYLKFFQFLVLASLSHFCSGVIHVTKEVKEVATLSCGLNVSVEELAQTRIYWQKGKKMVLTMMSGD
SEQ:223_ctla5x6f6 (1) MGYTRRQGTSPSKCPYLKFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTPIYWQKEKKMVLTMMSGD
SEQ:224_ctla5x5h12 (1) MGYTRRQGISPSKCPYLKFFQLLVLASLSHFCSGVIHVTKKVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:225_ctla5x5c10 (1) MSHTQRQGISPSKCPYLNFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD

Fig. 3A


Signal sequence
Extracellular domain (ECD)
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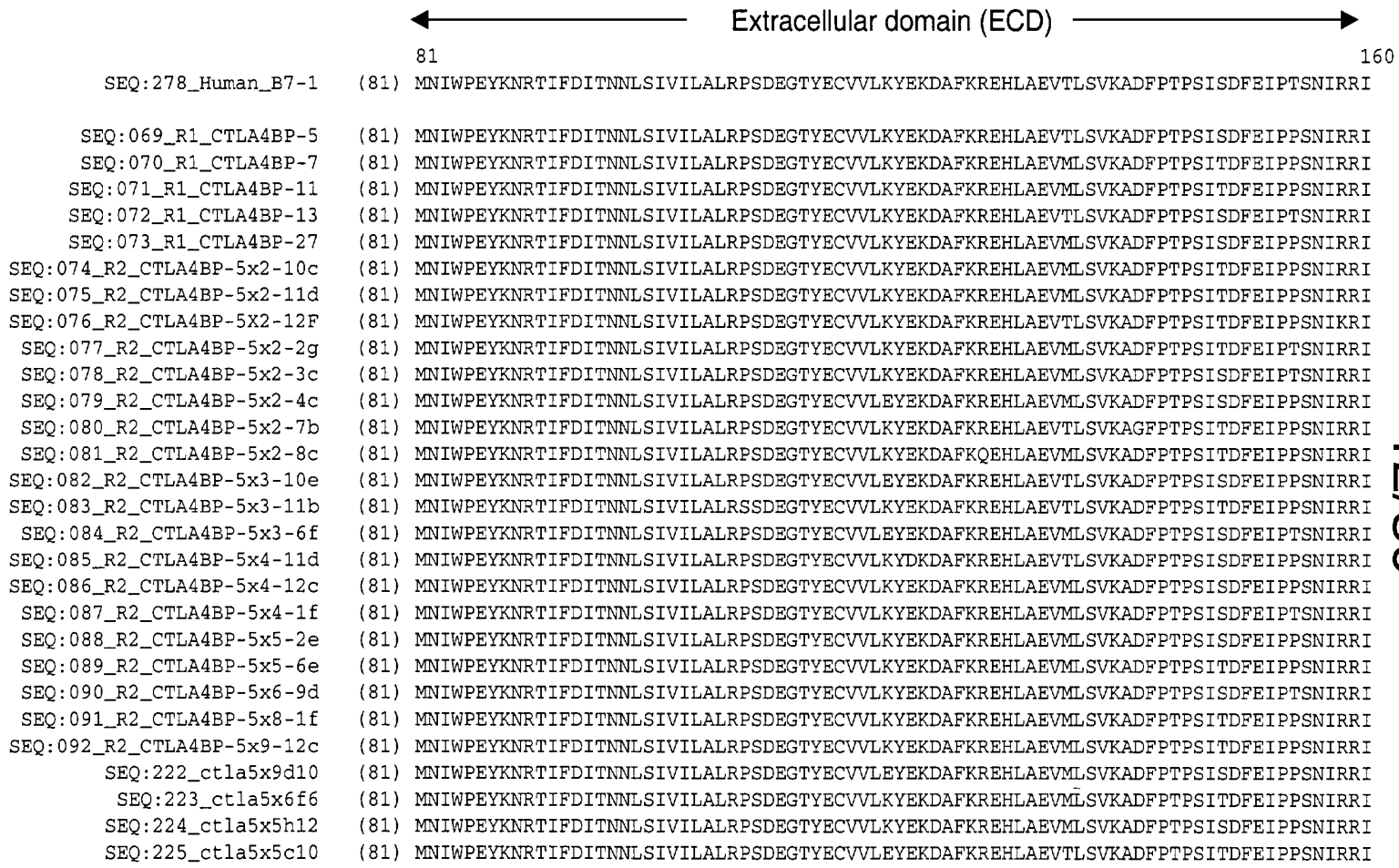
SEQ:226_ctla5x3e8 (1) MGHTRRQGTSPSKCPYLKFFQLLVLAGLSHLCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:227_ctla5x3c4 (1) MSHIRRQGISPSKCPYLNFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:228_ctla5x3c3 (1) MSHTRRQGTSPSKCPYLKFFQLLVLASLSHFCSGVIHMTKEVKEVATLSCGPNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:229_ctla5x2h11 (1) MSHTRRQGISSSKCPYLKFFQLLVLACLSHFCSGVIHVTKKVKEVATLSCGHNVSVEELAQTRIYWQKGKKMVLTMMSGD
SEQ:230_ctla5x2d7 (1) MGYTRRQGTSPSECPYLKFFQLLVLAGLSHFCSGVIHMTKEVKEVATLSCGLNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:231_ctla5x2b7 (1) MSHTRRQGISPSKCPYLNFFRLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:232_ctla5x2b1 ns (1) MSHTRRQGISPSKCPYLKFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:233_ctla5x1f1 (1) MGHTRRQGISPSKCPYLKFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGLNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:234_ctla5x1d7 (1) MGYTRRQGTSPSKCPYLNFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVPVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:235_ctla2x4g9 (1) MGHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKDKKMVLTMMSGD
SEQ:236_ctla2x4a6 (1) MGHTRRQGTSPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:237_ctla2x2f3 (1) MGHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIYVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLIMMSGD
SEQ:238_ctla2x2f12 (1) MGHTRRQGTSPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:239_ctla2x1g8 (1) MGYTRRQGTSPSKCPYLNFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:240_ctla2x1f10 (1) MGYTRRQGISPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:241_ctla2x1c9 (1) MSHTRRQGISPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSAEELAQTRIYWQKEKKMVLTMMSGD
SEQ:242_ctla2x1h12 (1) MGHTRRQGISPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGLNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:243_ctla2x1e2 (1) MGYTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSDEELAQTRIHWQKEKKMVLTMMSGD
SEQ:244_ctla2x1c4 (1) MGYTRRQGISPSKCPYLKFFQLLVLAGLSHLCSGVIHVTKEVKEVATLPCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:245_ctla2x1b12 (1) MGHTRRQGISPSKCPYLKFFQLLVLAGLSHLCSGVIHMTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:246_ctla2x2f1 (1) MGHTRRQGISPSKCPYLKFFQLLGLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:247_ctla5x4h1 (1) MSHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:248_ctla5x4a1 (1) MGHTRRQGTSPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:249_ctla5x2f3 (1) MSHTRRQGISPSKCPYLKFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMPGD
SEQ:250_ctla5x2e12 (1) MSHTRRQGISPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGG
SEQ:251_ctla2x4h11 (1) MGYTRRQGTSPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:252_ctla2x3h2 (1) MGHTRRQGTSPSKCPYLNFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:286_CTLA4BP_Con (1) MGHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD

Fig. 3B


Extracellular domain (ECD)
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SEQ:069_R1_CTLA4BP-5 (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPPSNIRRI
SEQ:070_R1_CTLA4BP-7 (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:071_R1_CTLA4BP-11 (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:072_R1_CTLA4BP-13 (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNIRRI
SEQ:073_R1_CTLA4BP-27 (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
SEQ:074_R2_CTLA4BP-5x2-10c (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:075_R2_CTLA4BP-5x2-11d (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:076_R2_CTLA4BP-5X2-12F (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSITDFEIPPSNIKRI
SEQ:077_R2_CTLA4BP-5x2-2g (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPTSNIRRI
SEQ:078_R2_CTLA4BP-5x2-3c (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPTSNIRRI
SEQ:079_R2_CTLA4BP-5x2-4c (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLEYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
SEQ:080_R2_CTLA4BP-5x2-7b (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKAGFPTPSITDFEIPPSNIRRI
SEQ:081_R2_CTLA4BP-5x2-8c (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKQEHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:082_R2_CTLA4BP-5x3-10e (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLEYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPPSNIRRI
SEQ:083_R2_CTLA4BP-5x3-11b (81) MNIWPEYKNRTIFDITNNLSIVILALRSSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSITDFEIPPSNIRRI
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Fig. 3C

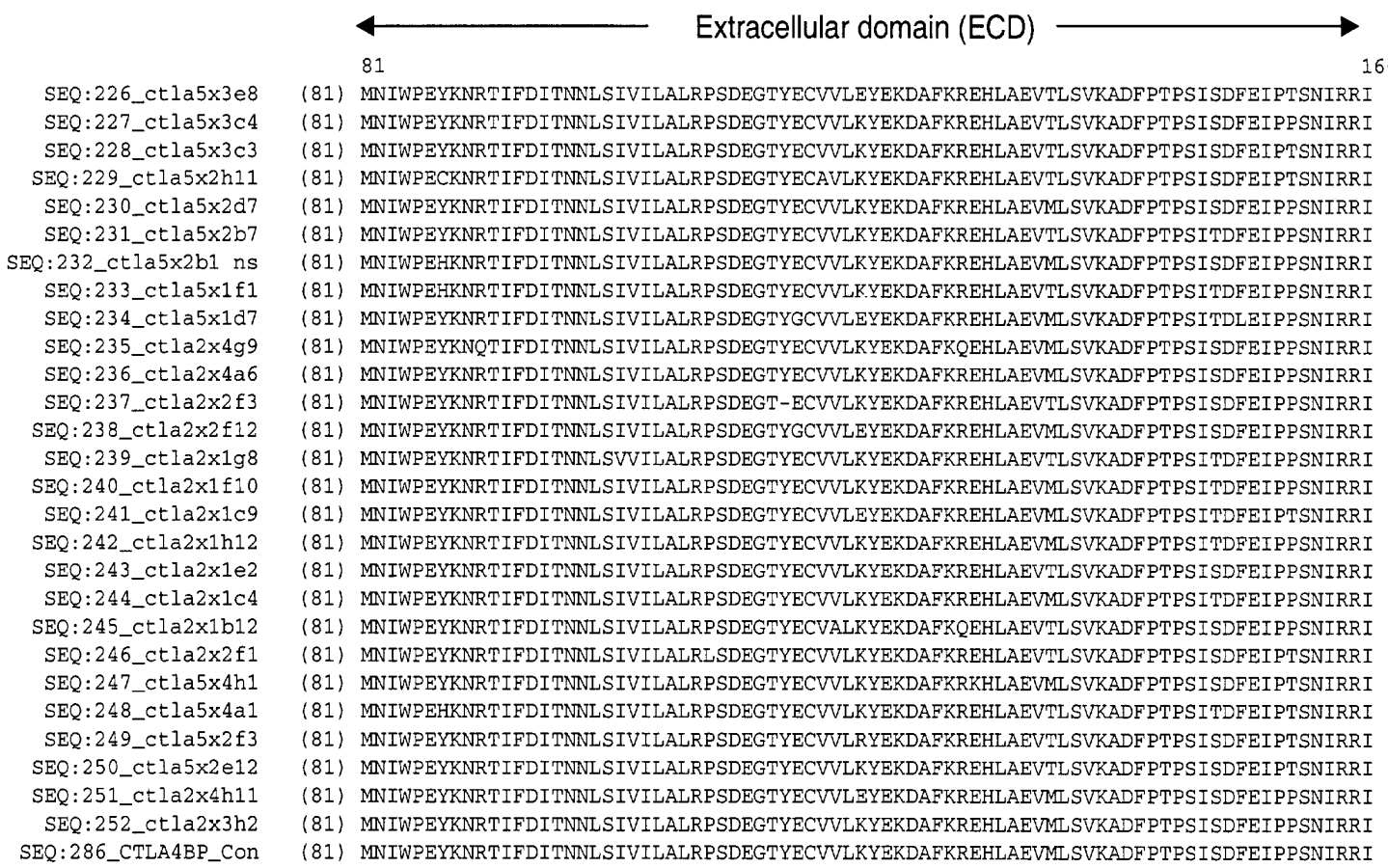
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Fig. 3D

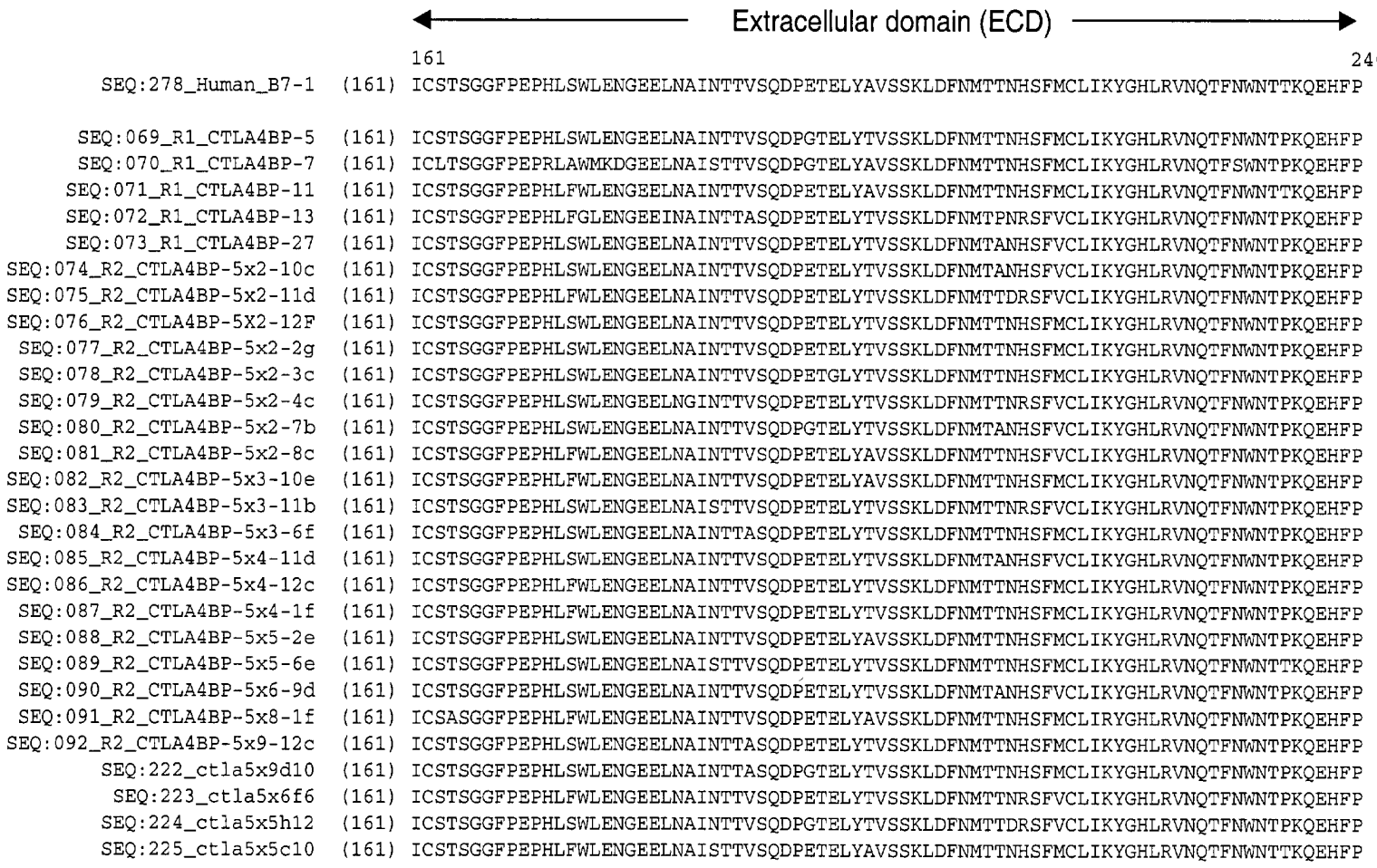
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Fig. 3E

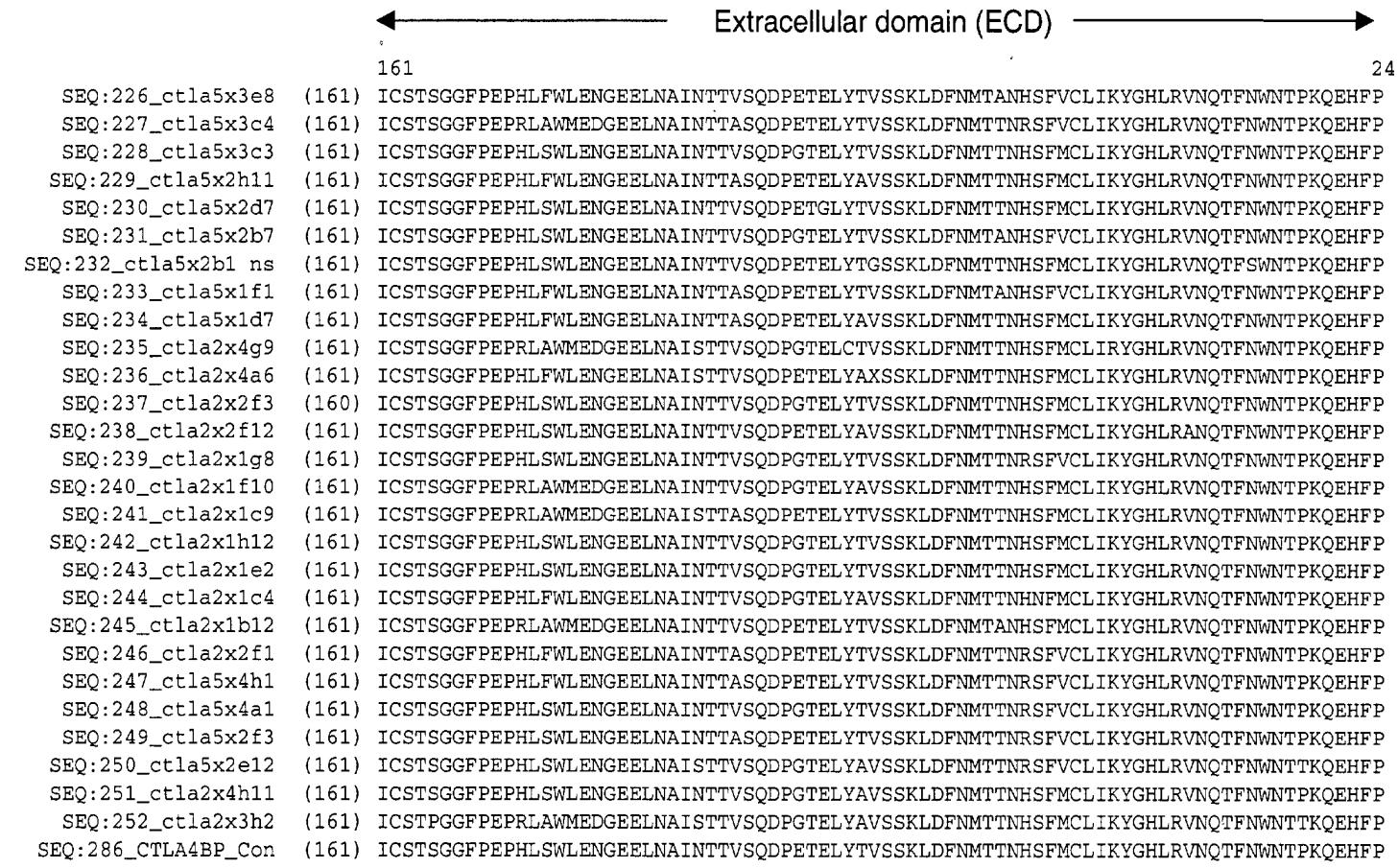
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Fig. 3F

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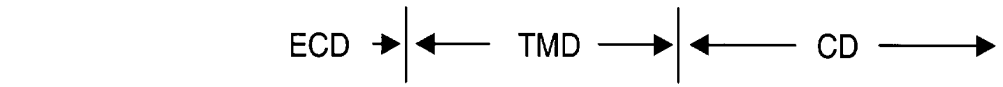
Fig. 3G

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   SEQ:227_ctla5x3c4  (241) DNLFPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
   SEQ:228_ctla5x3c3  (241) DNLLPSWAITLISVNGIFVICCLTHCFAPRCRERRRNERLRRESVCPV
  SEQ:229_ctla5x2h11  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERKSNERLRRESVRPV
   SEQ:230_ctla5x2d7  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
   SEQ:231_ctla5x2b7  (241) DNLLPSWAITLISANGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
SEQ:232_ctla5x2b1 ns  (241) DNLLPSWAITLISANGIFVICCLTYCFAPRCRERRRNETLRRESVRPVWGTKLKFKPXIS
   SEQ:233_ctla5x1f1  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNETLRRESVRPV
   SEQ:234_ctla5x1d7  (241) DNLLPSWAITLISANGIFVICCLTYCFAPRCRERRRNERLRRESVHPV
   SEQ:235_ctla2x4g9  (241) DNLLPSWAITLISVKGIFVICCLTYCFAPRGRERKSNGRLRRESVHPV
   SEQ:236_ctla2x4a6  (241) DNLLPSWAITLISVNGIFVICCPTYCFAPRCRERRRNERLRRESVCPV
   SEQ:237_ctla2x2f3  (240) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVCPV
  SEQ:238_ctla2x2f12  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
   SEQ:239_ctla2x1g8  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERKSNERLRRESVRPV
  SEQ:240_ctla2x1f10  (241) DNLLPSWAITLISVNGISVICCLTYCFAPRCRERRRNERLRRESVCPV
   SEQ:241_ctla2x1c9  (241) DNLLPSWAITLISVNGIFVICCLTHCFAPRCRERRRNERLRRESVCPV
  SEQ:242_ctla2x1h12  (241) DNLLPSWAITLISANGIFVICCLTYCFAPRCRERKSNERLRRESVCPV
   SEQ:243_ctla2x1e2  (241) DNLLPS-AITLISANGIFVICCLTYCFAPRCRERRRNERLRRESIHPV
   SEQ:244_ctla2x1c4  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
  SEQ:245_ctla2x1b12  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVCPV
   SEQ:246_ctla2x2f1  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
   SEQ:247_ctla5x4h1  (241) NNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNETLRRESVHPV
   SEQ:248_ctla5x4a1  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
   SEQ:249_ctla5x2f3  (241) DNLLPSWAITLISANGIFVICCLTHCFAPRCRERKSNERLRRESVRPV
  SEQ:250_ctla5x2e12  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
  SEQ:251_ctla2x4h11  (241) DNLLPSWAITLISVNGIFVICCLAYCFAPRCRGRRRNERLRRESVRPV
   SEQ:252_ctla2x3h2  (241) DNLLPSWAITLISVKGIFVICCLTYCFAPRWRERKSNERLRRESVRPV
 SEQ:286_CTLA4BP_Con  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
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Fig. 3H

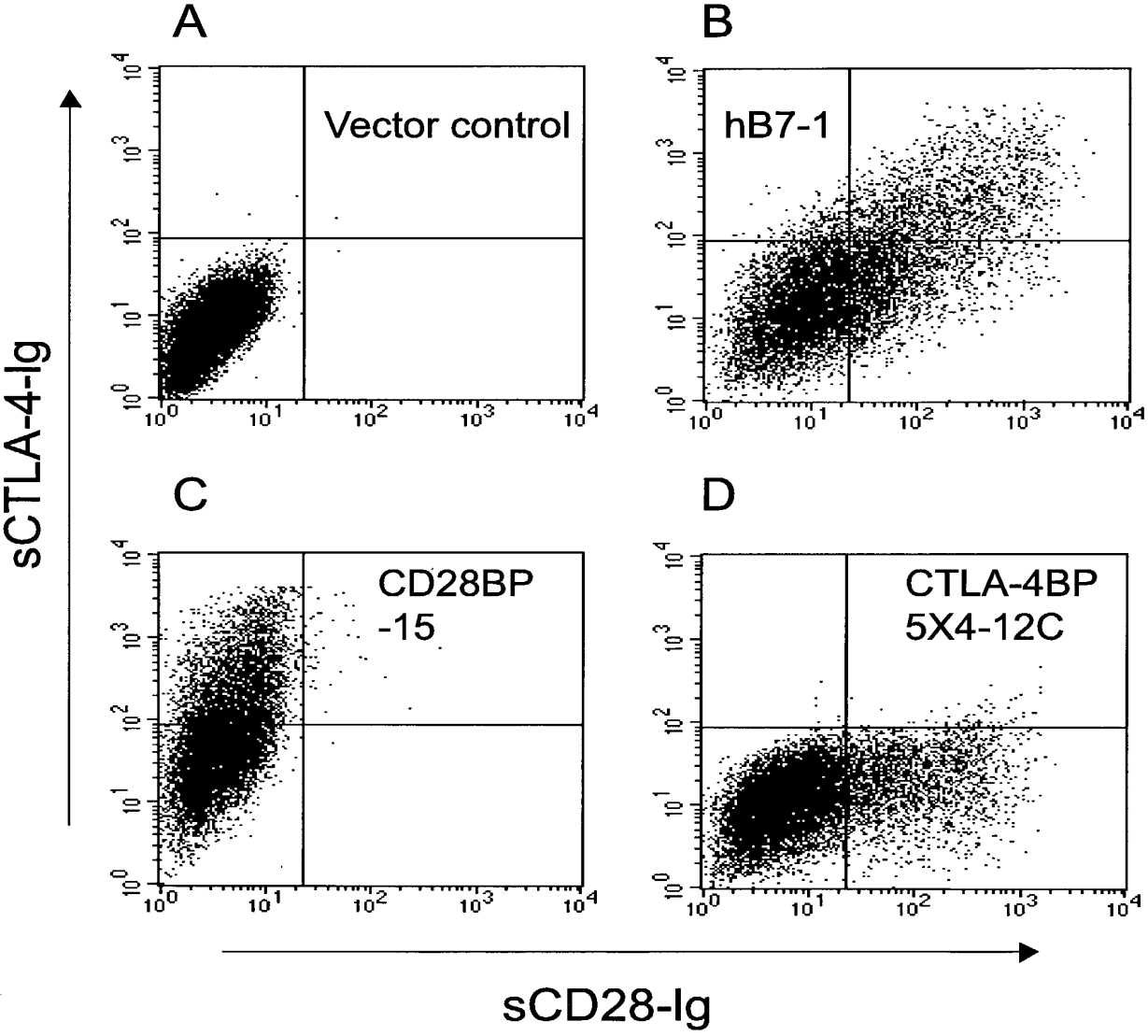

A
Vector control
B
hB7-1
C
CD28BP
-15
D
CTLA-4BP
5X4-12C
sCTLA-4-Ig
sCD28-Ig

Fig. 4

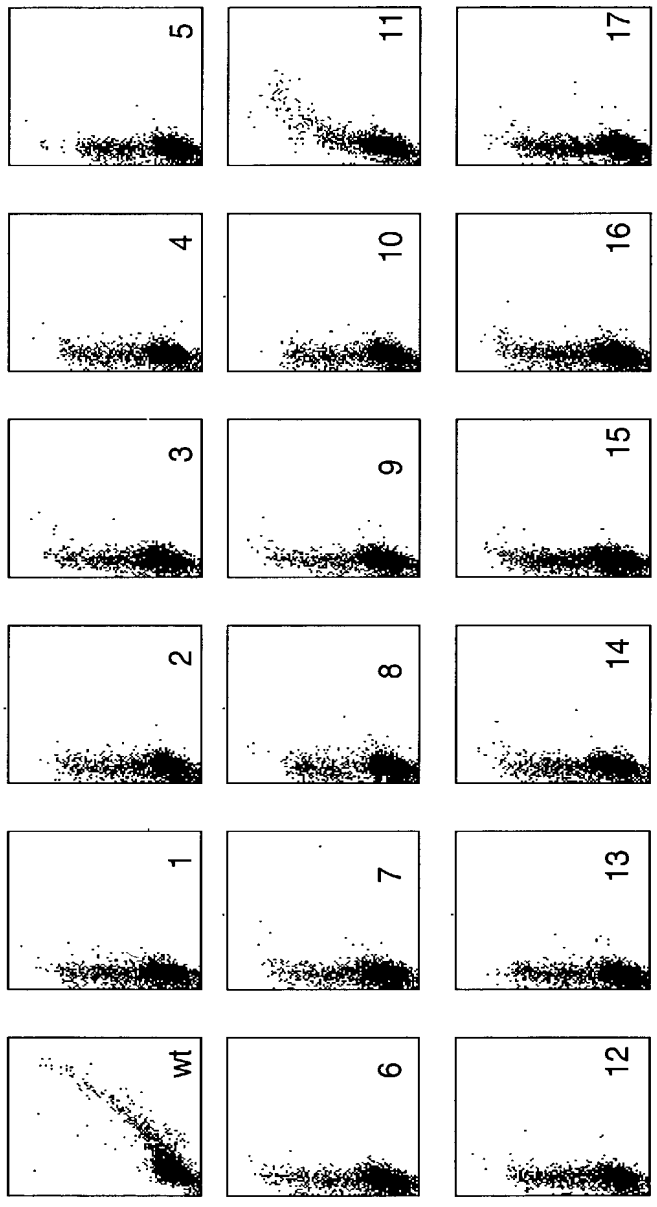

wt
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
CD28 Binding
CTLA4 Binding

Fig. 5

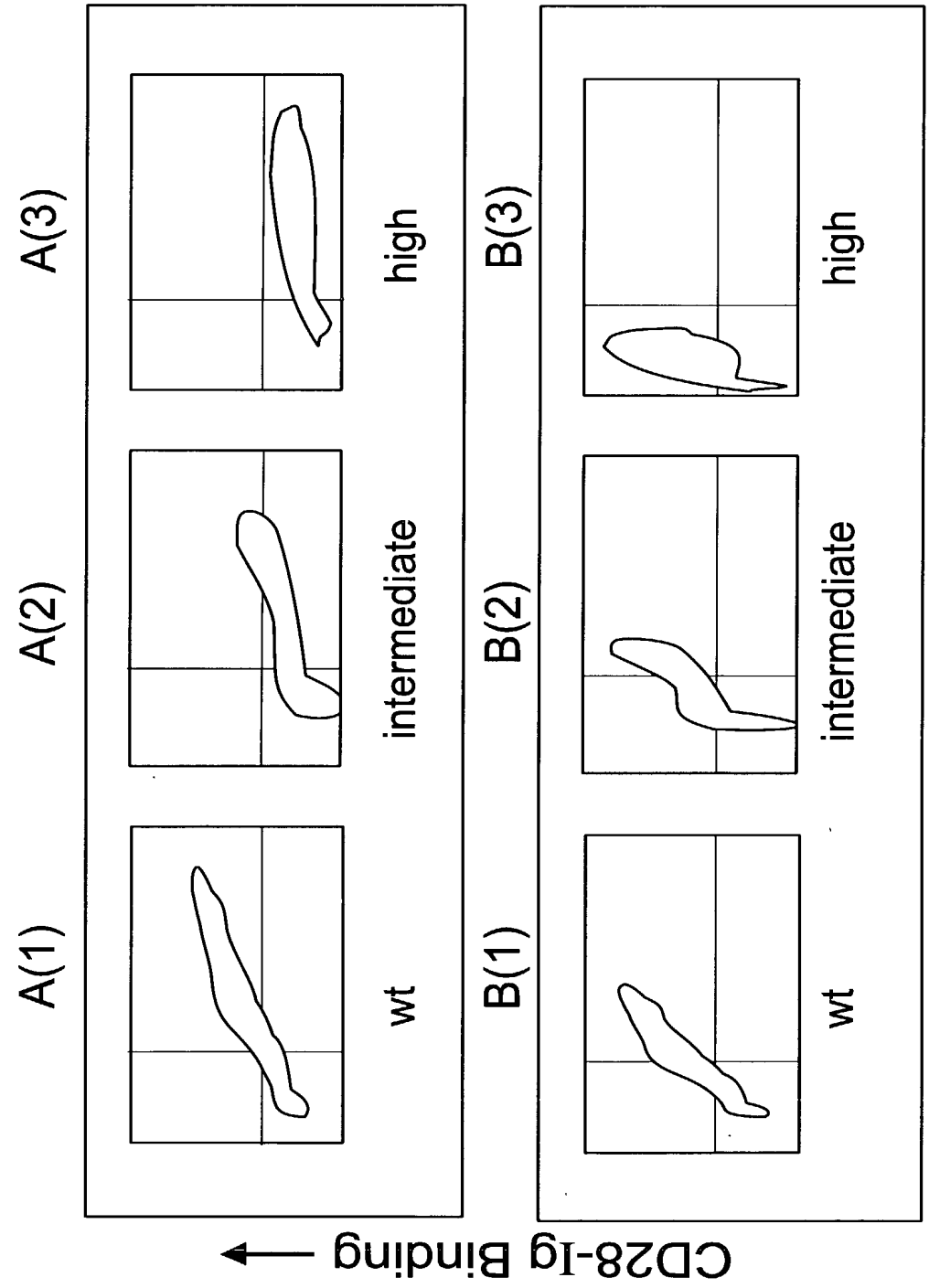

A(1)
A(2)
A(3)
wt
intermediate
high
B(1)
B(2)
B(3)
wt
intermediate
high
CD28-Ig Binding
CTLA-4-Ig Binding

Fig. 6

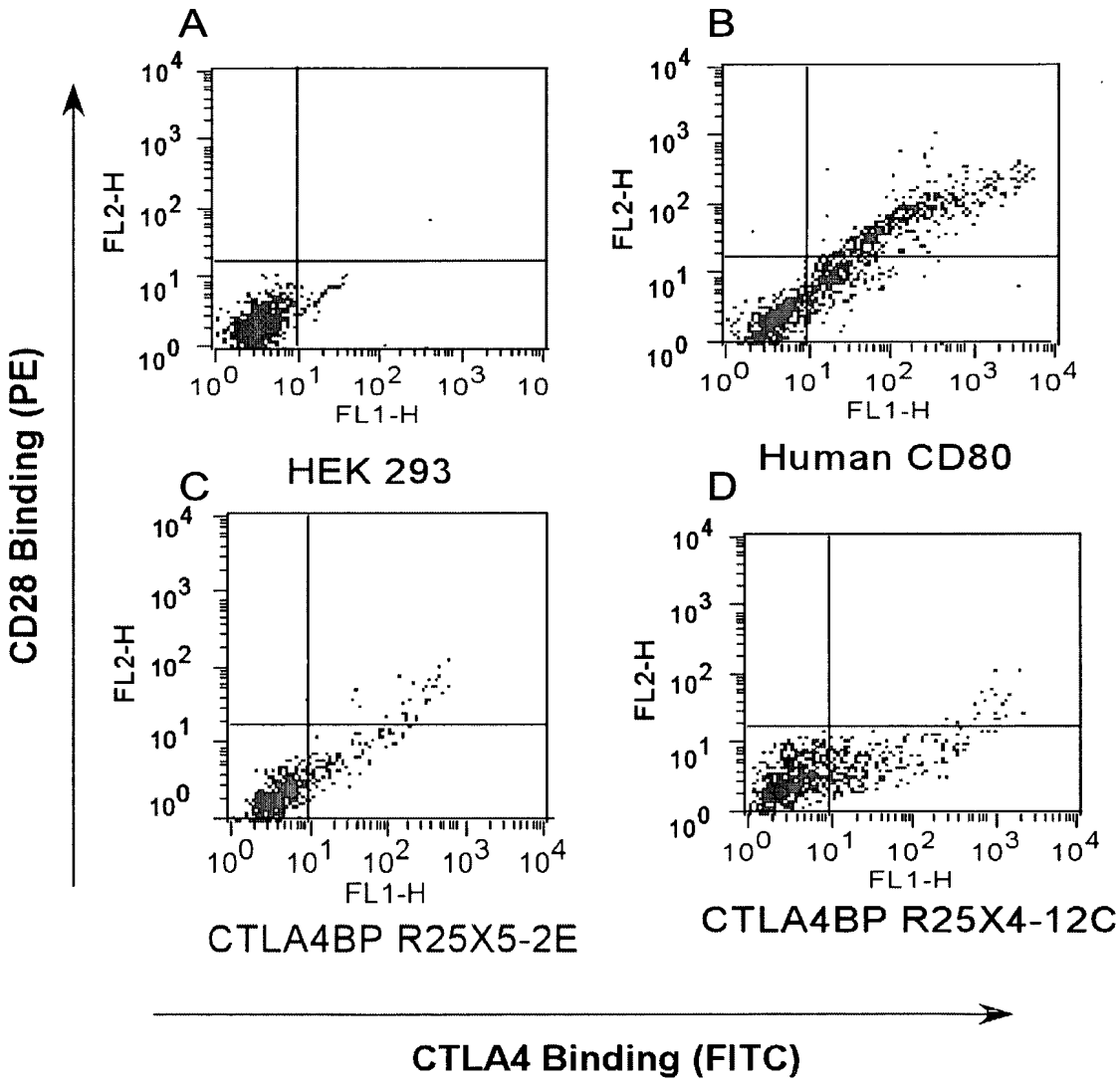

A
B
C
D
HEK 293
Human CD80
CTLA4BP R25X5-2E
CTLA4BP R25X4-12C
FL2-H
FL1-H
CD28 Binding (PE)
CTLA4 Binding (FITC)

Fig. 7A-D

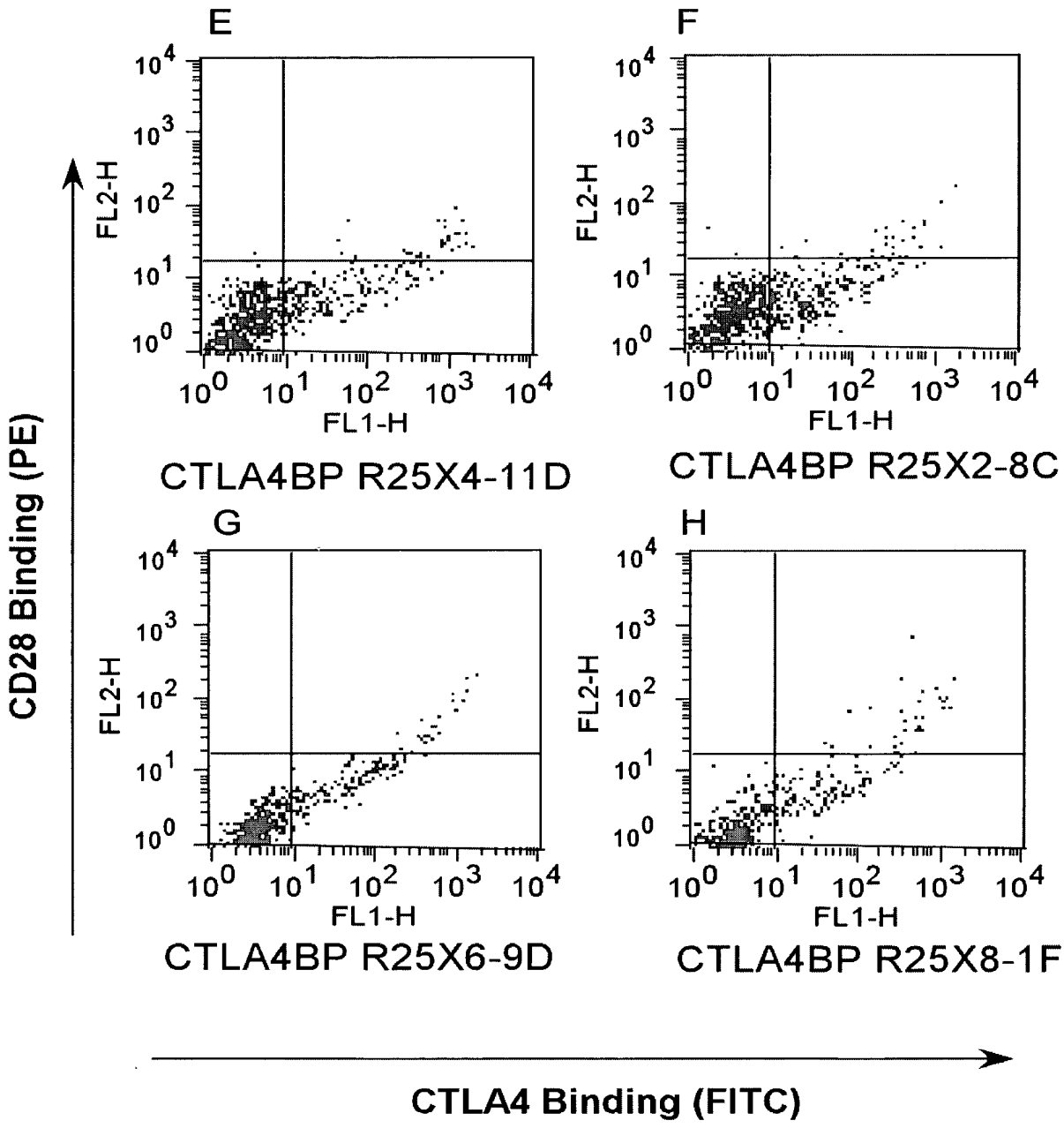

E
F
G
H
FL2-H
FL1-H
CD28 Binding (PE)
CTLA4 Binding (FITC)
CTLA4BP R25X4-11D
CTLA4BP R25X2-8C
CTLA4BP R25X6-9D
CTLA4BP R25X8-1F

Fig. 7E-H

Fig. 8A

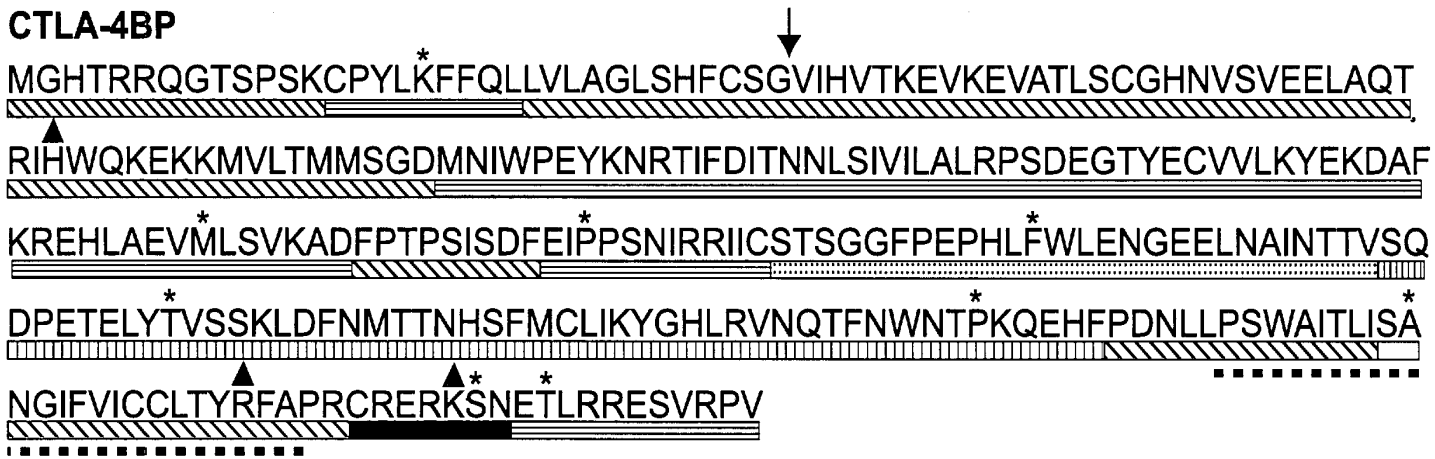

CTLA-4BP
MGHTRRQGTSPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQT
RIHWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAF
KREHLAEVMLSVKADFPTPSISDFEIPPSNIRRIICSTSGGFPEPHLFWLENGEELNAINTTVSQ
DPETELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFPDNLLPSWAITLISA
NGIFVICCLTYRFAPRCRERKSNETLRRESVRPV

Fig. 8B


CD28BP
MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELT
SLRIYWQKDSKMVLAILPGKVQVWPEYKNRTITDMNDNPRIVILALRPSDSGTYTCVIQKPVLK
GAYKLEHLASVRLMIRADFPVPTINDLGNPSPNIRRLICSTSGGFPRPHLYWLENGEELNATNT
TVSQDPGTELYMISSELDFNVTNNHSIVCLIKYGELSVSQIFPWSKPKQEPPIDQLPFWVIIPVS
GALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
human
orangutan
rhesus
baboon
rhesus/baboon
cow
rabbit

Vector control
hB7-1
hB7-1-Flag
CD28BP-15
CD28BP-Flag
CTLA-4BP 5X4-12c

Fig. 9A

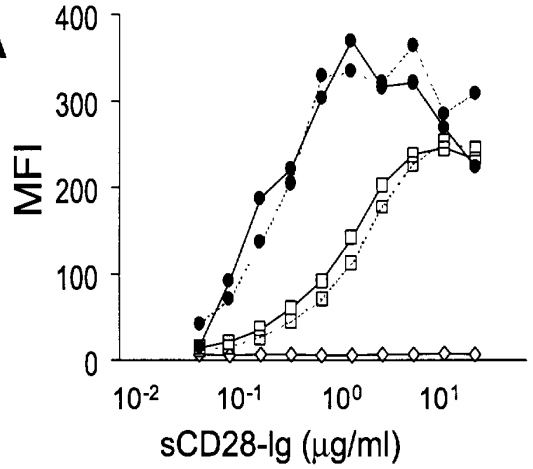


Fig. 9B

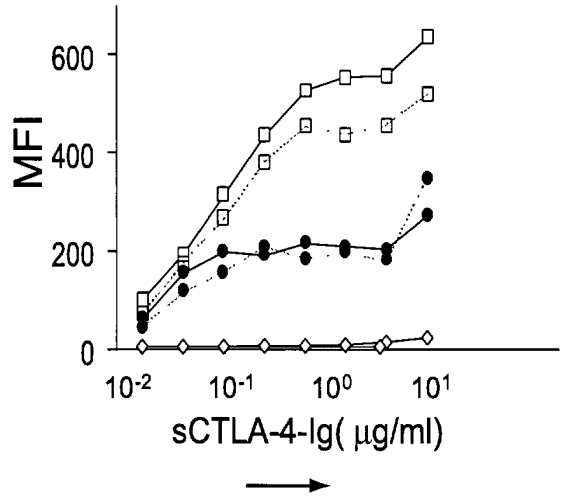


Fig. 9C

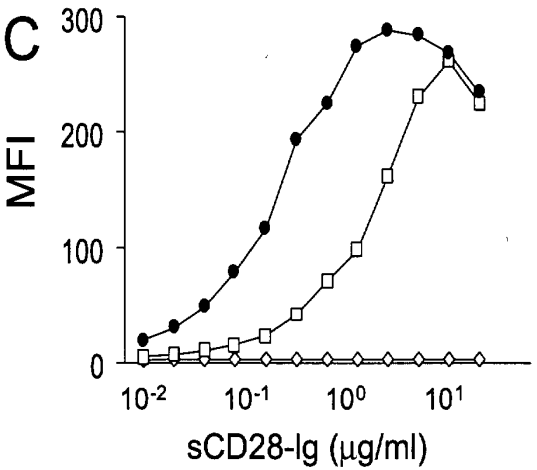


Fig. 9D

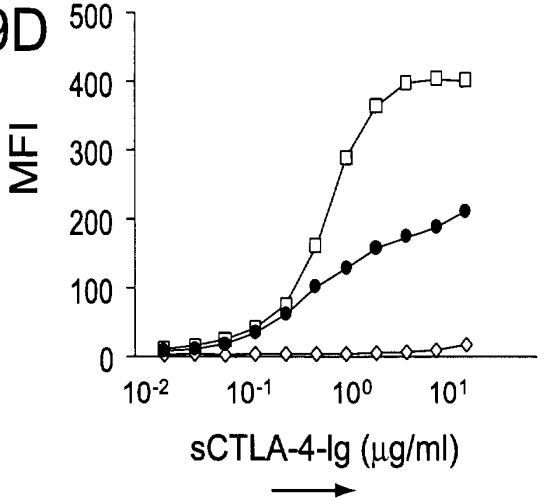


Fig. 9E

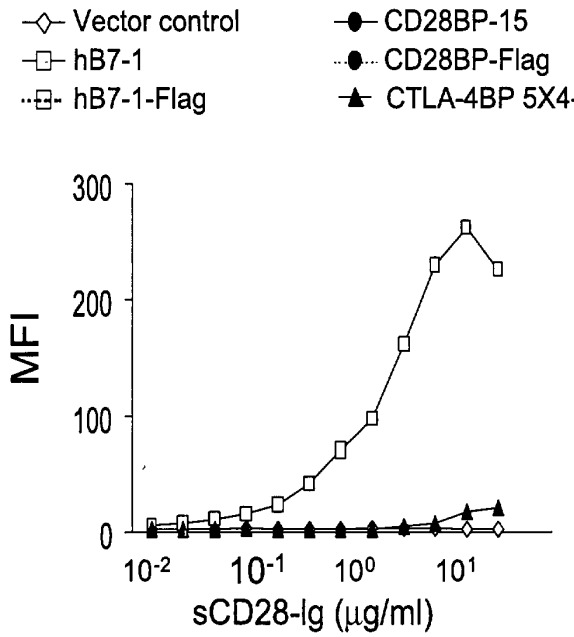


Fig. 9F

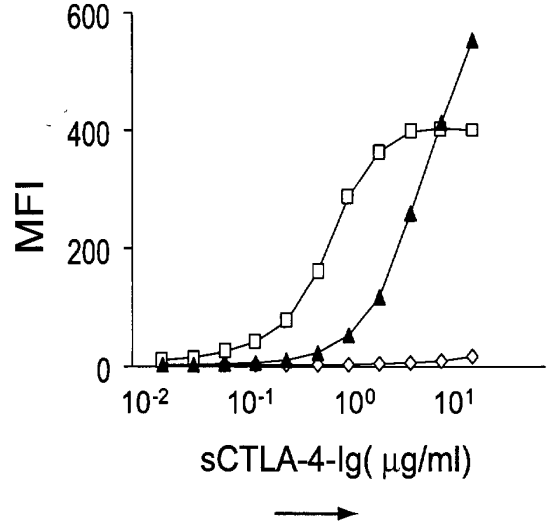


Fig. 9G

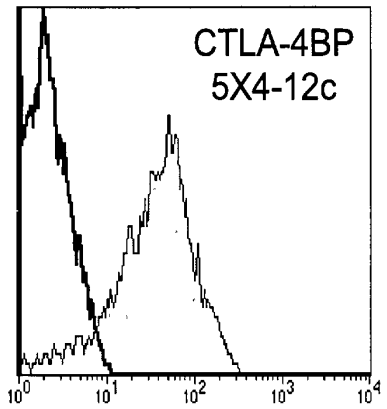
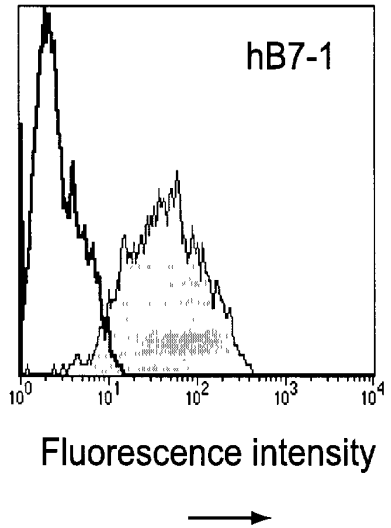


Fig. 9H



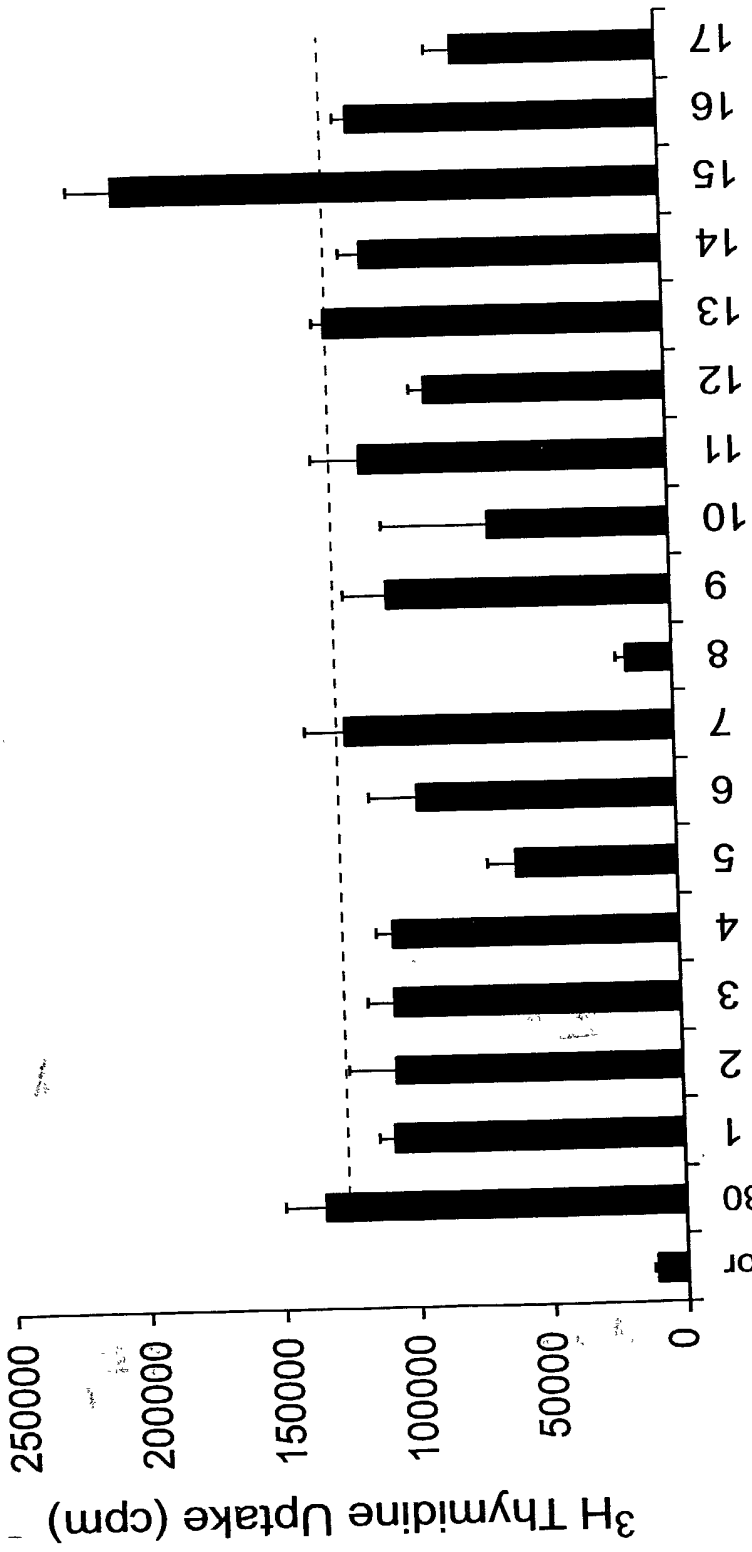

3H Thymidine Uptake (cpm)
250000
200000
150000
100000
50000
0
Control Vector
(B7-1) CD80
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
CD28BP Clone Number

Fig. 10

Fig. 11A

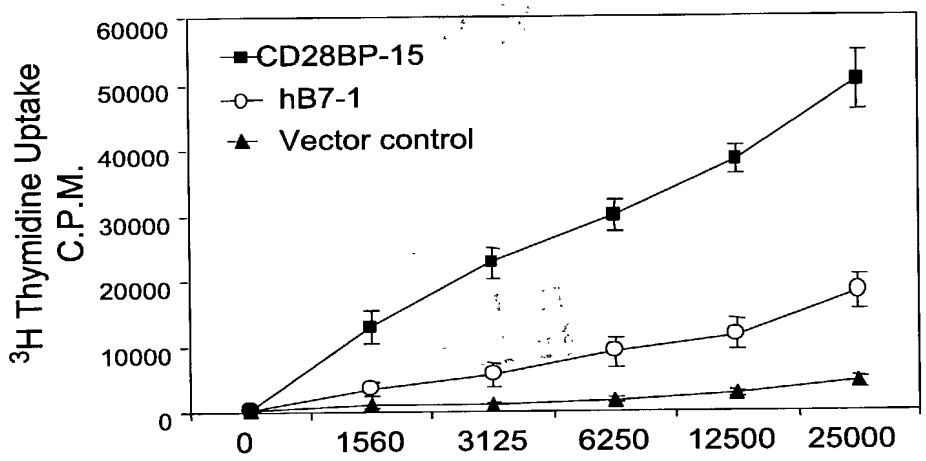


Fig. 11B

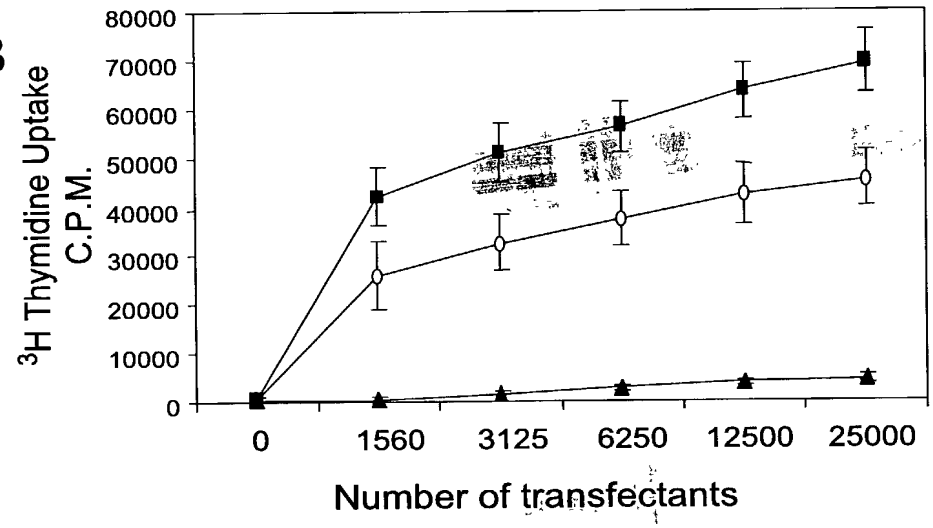
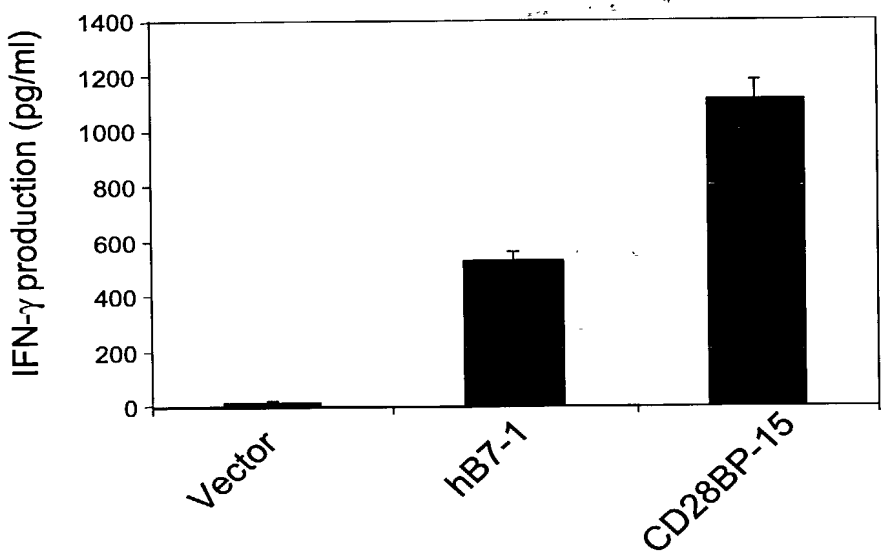


Fig. 11C



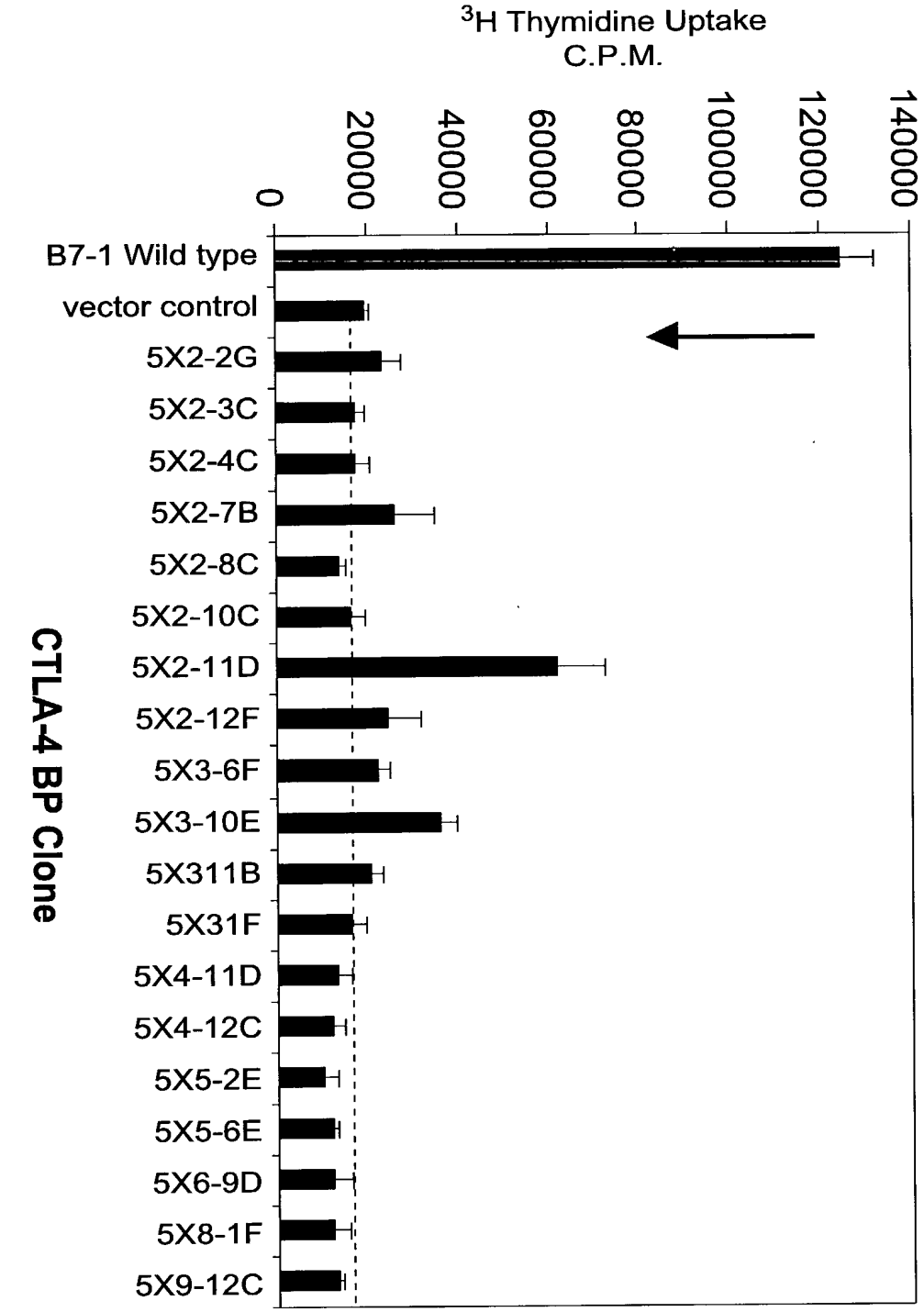

^{3}H Thymidine Uptake
C.P.M.
0
20000
40000
60000
80000
100000
120000
140000
B7-1 Wild type
vector control
5X2-2G
5X2-3C
5X2-4C
5X2-7B
5X2-8C
5X2-10C
5X2-11D
5X2-12F
5X3-6F
5X3-10E
5X311B
5X31F
5X4-11D
5X4-12C
5X5-2E
5X5-6E
5X6-9D
5X8-1F
5X9-12C
CTLA-4 BP Clone

Fig. 12

Fig. 13A

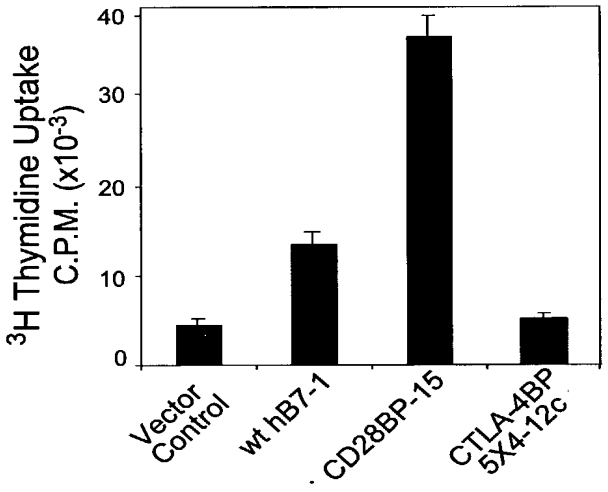


Fig. 13B

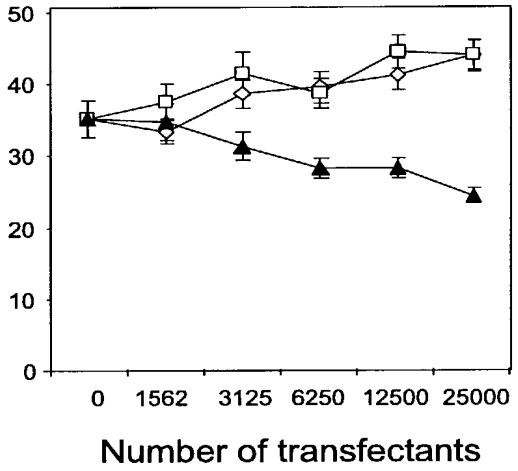


Fig. 13C

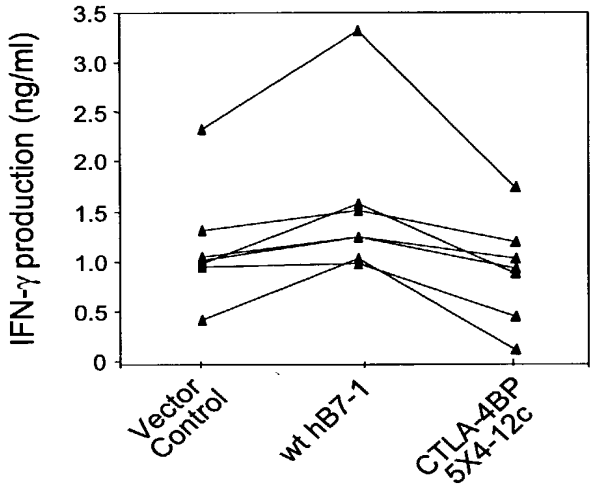


Fig. 13D

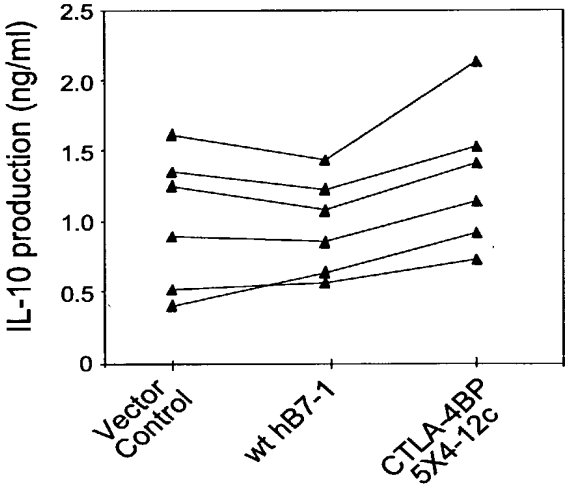


Fig. 14A

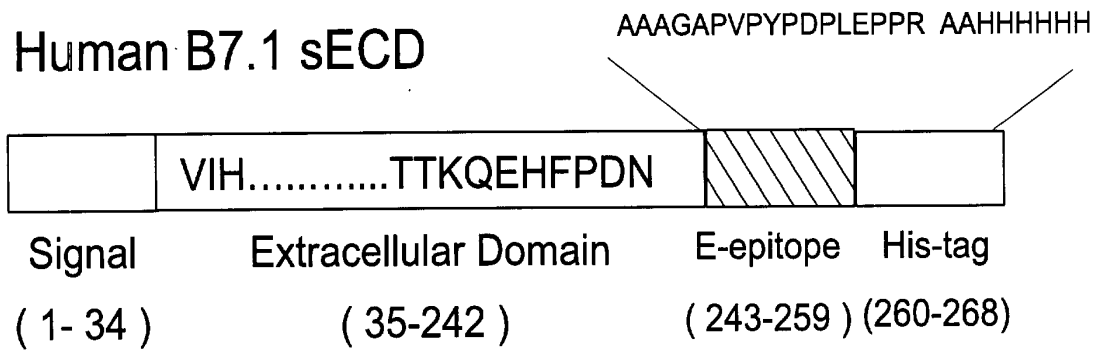
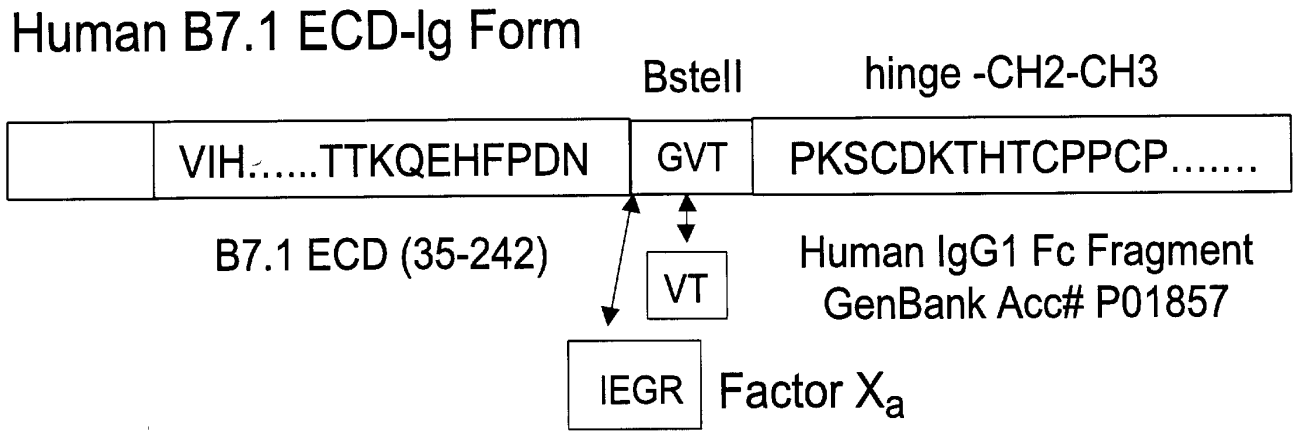


Fig. 14B



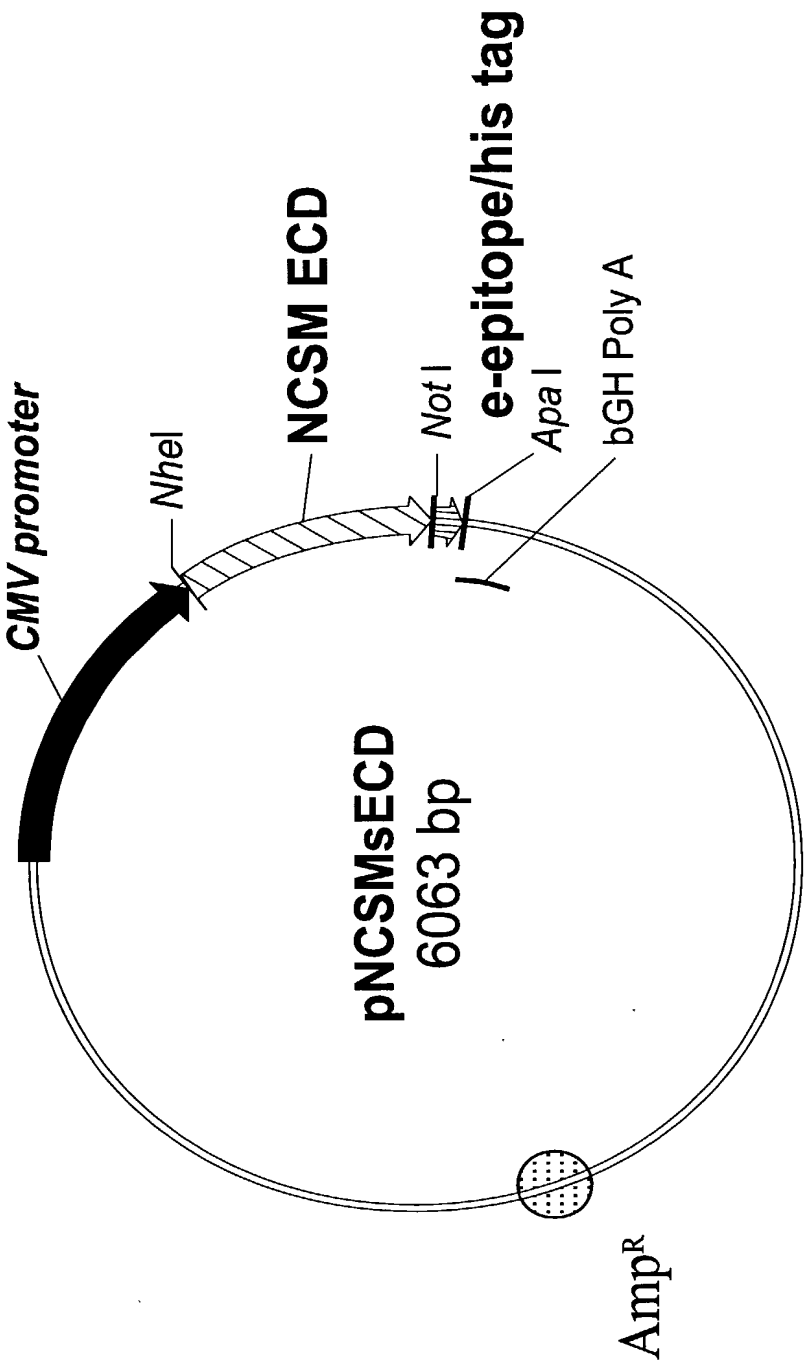

CMV promoter
NheI
NCSM ECD
NotI
e-epitope/his tag
ApaI
bGH Poly A
pNCSMsECD
6063 bp
AmpR

Fig. 15

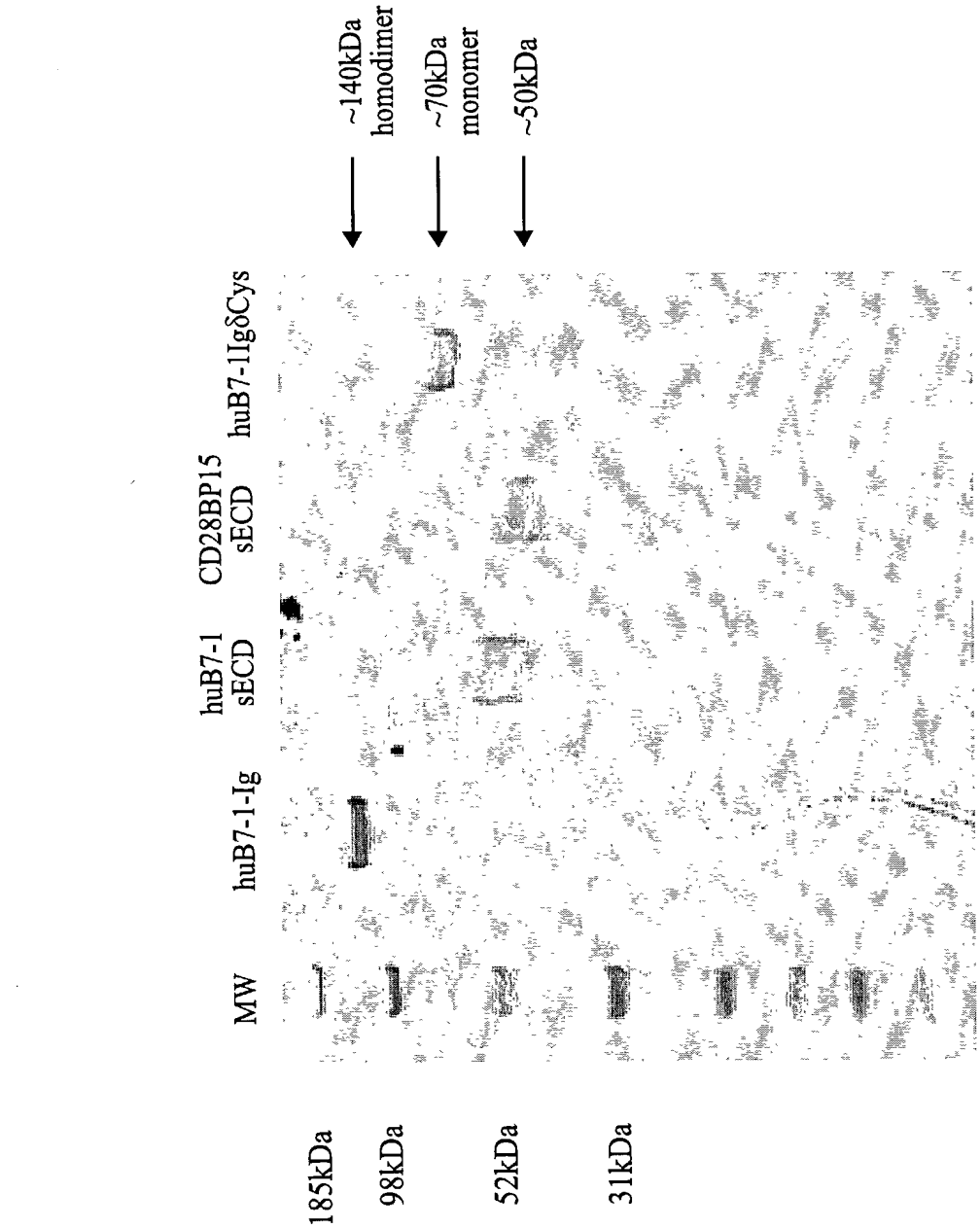

MW
huB7-1-Ig
huB7-1 sECD
CD28BP15 sECD
huB7-1IgδCys
185kDa
98kDa
52kDa
31kDa
~140kDa homodimer
~70kDa monomer
~50kDa

Fig. 16

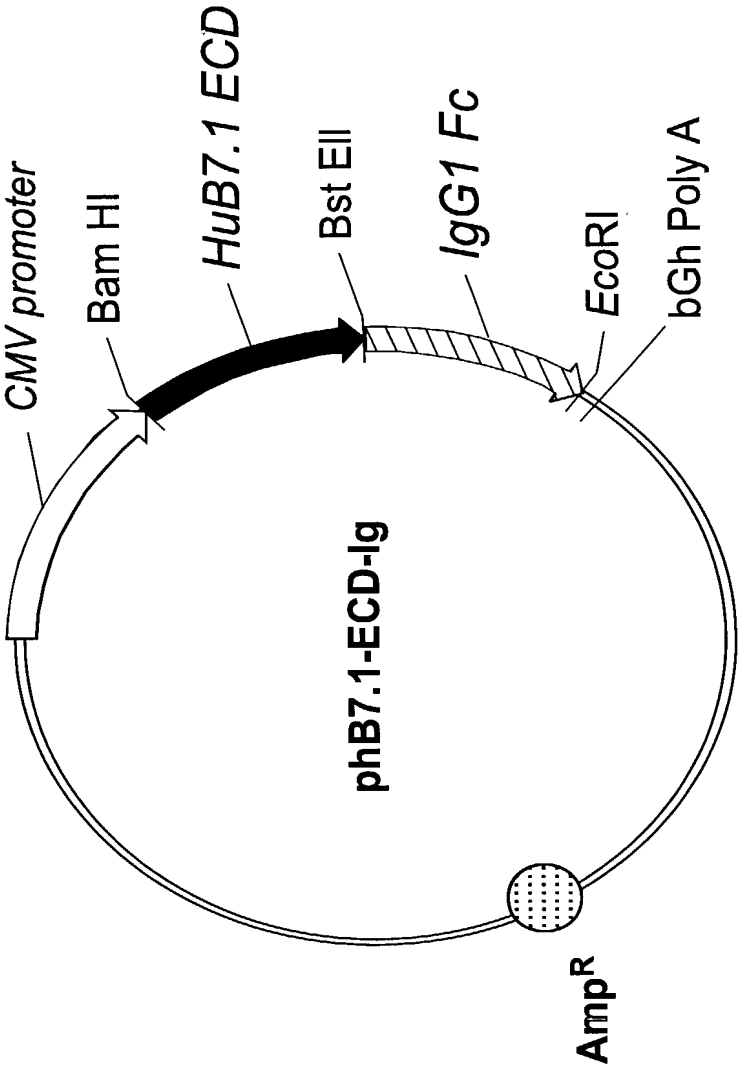

CMV promoter
Bam HI
HuB7.1 ECD
Bst EII
IgG1 Fc
EcoRI
bGh Poly A
phB7.1-ECD-Ig
AmpR

Fig. 17

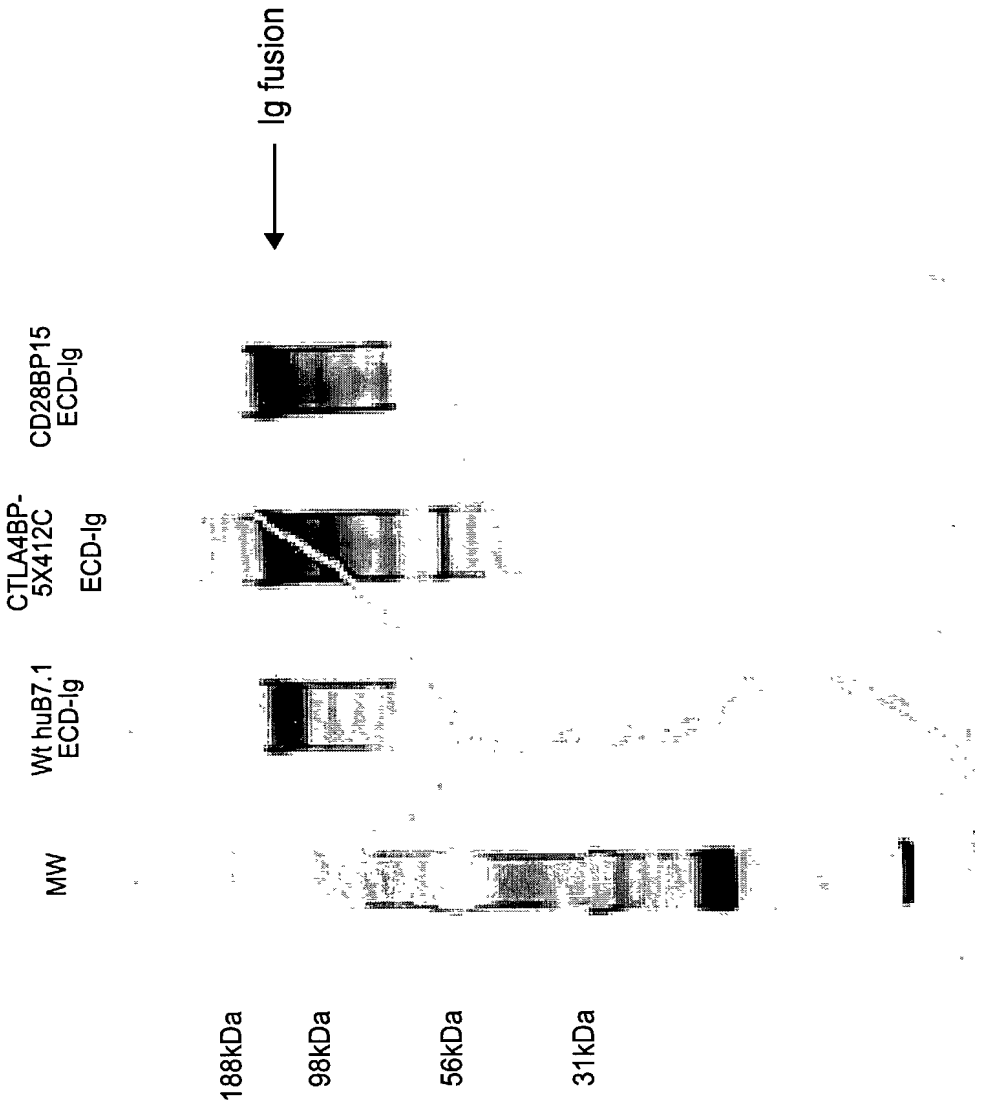

Ig fusion
CD28BP15 ECD-Ig
CTLA4BP-5X412C ECD-Ig
Wt huB7.1 ECD-Ig
MW
188kDa
98kDa
56kDa
31kDa

Fig. 18

Expression of CTLA-4BP-Ig and CD28BP-Ig Proteins

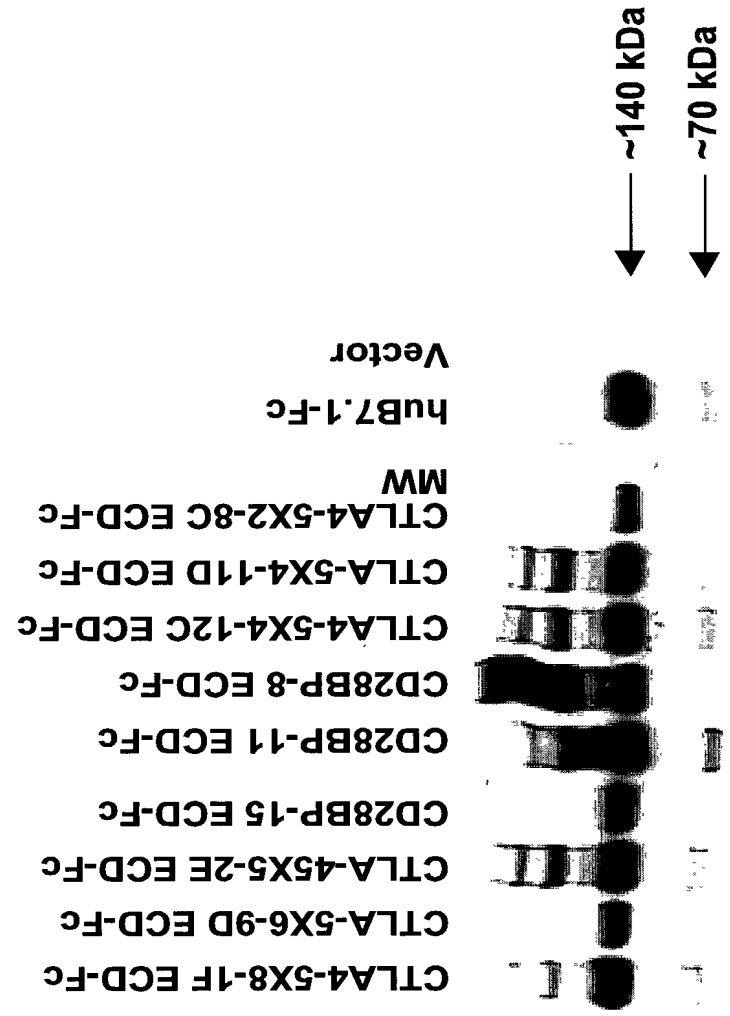


Fig. 19

Fig. 20A

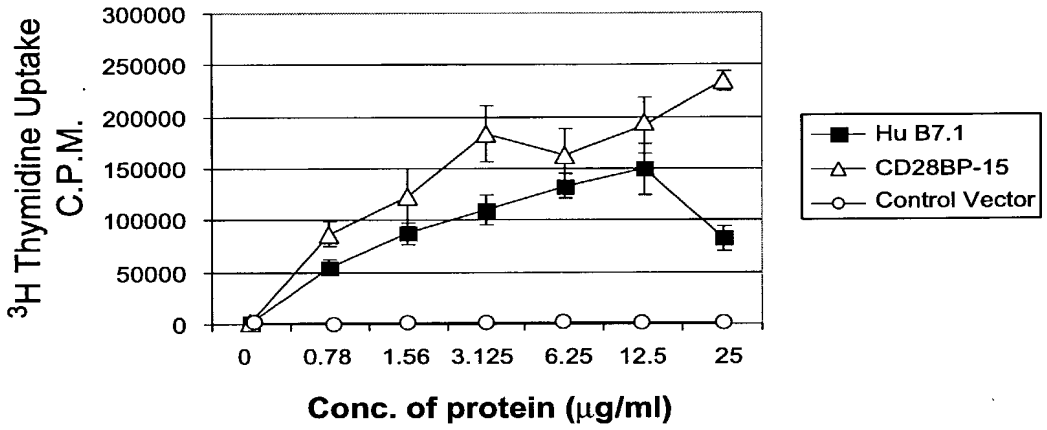


Fig. 20B

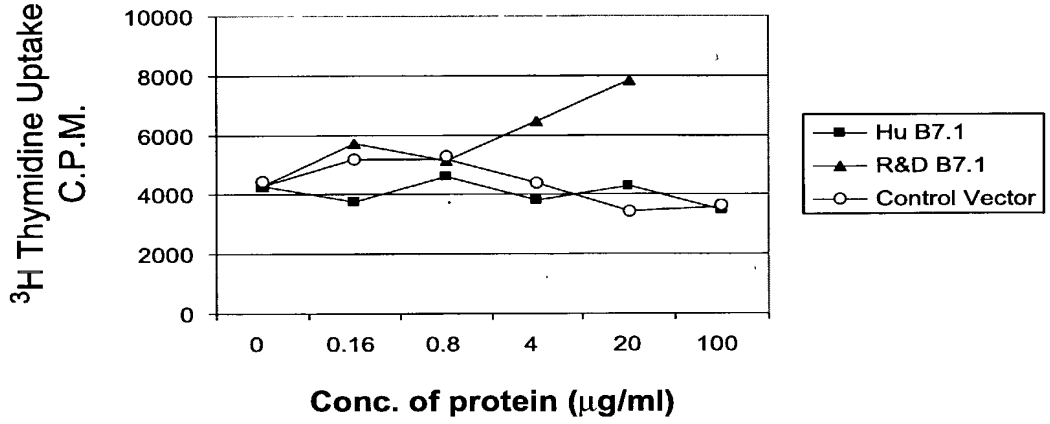


Fig. 20C

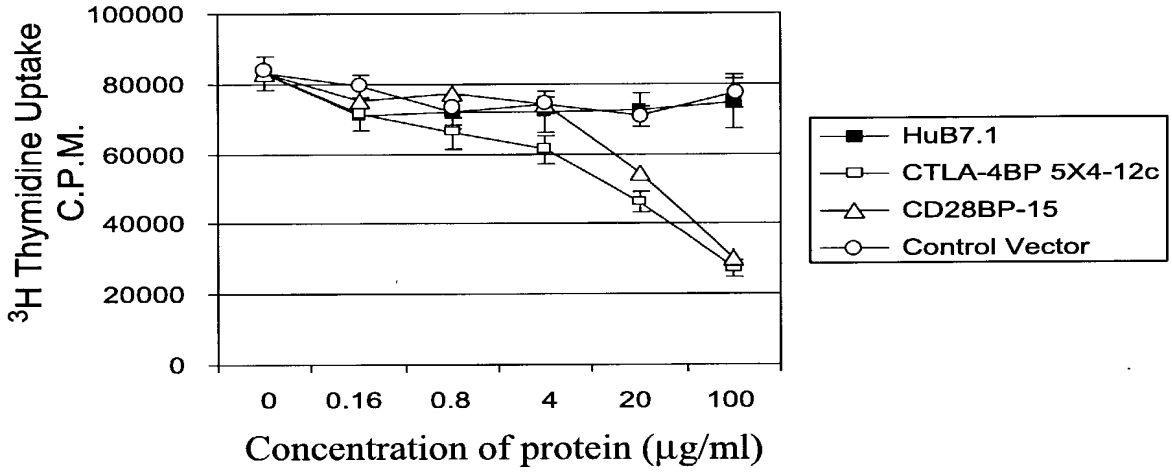
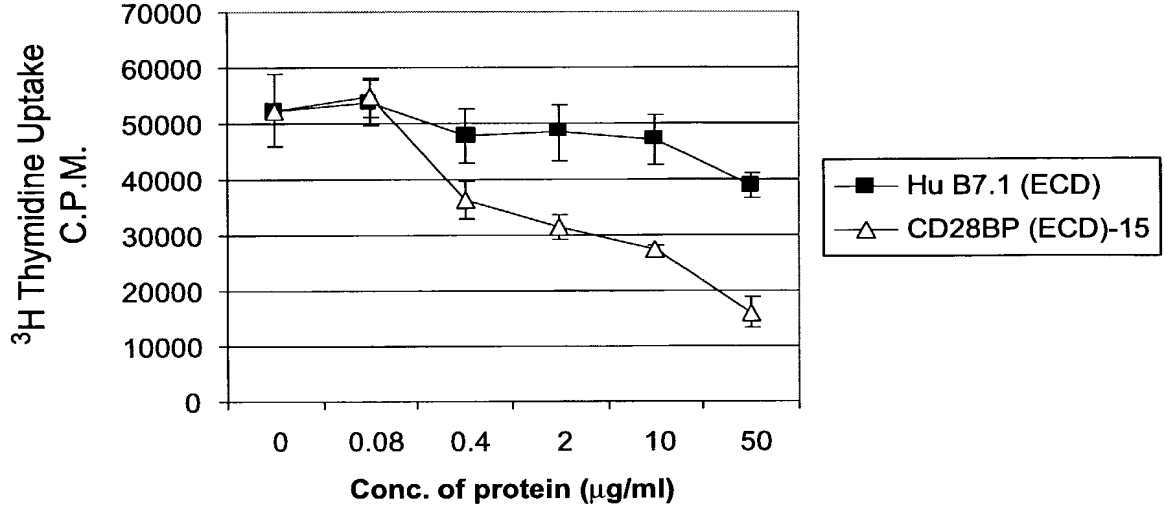


Fig. 20D



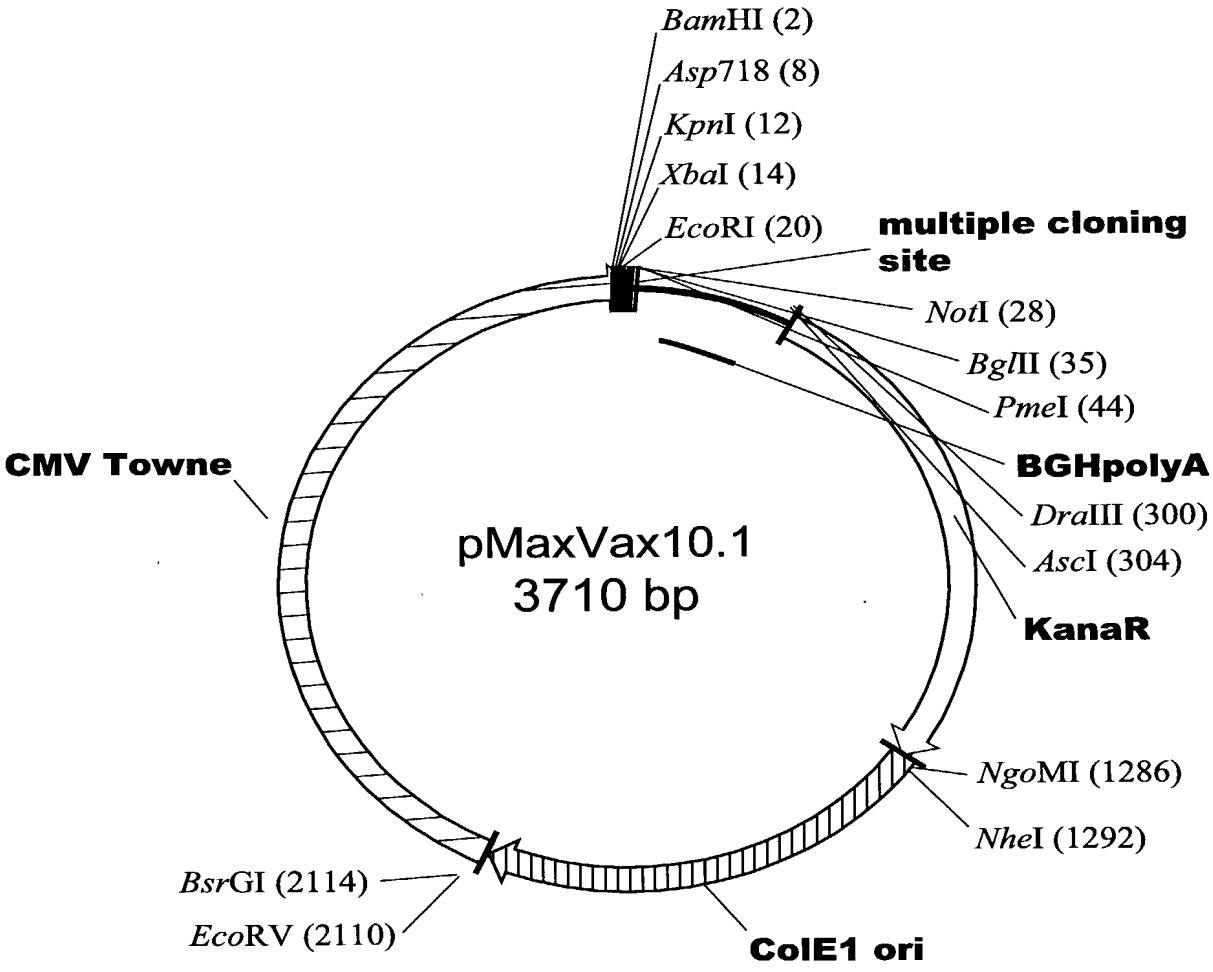

BamHI (2)
Asp718 (8)
KpnI (12)
XbaI (14)
EcoRI (20)
multiple cloning site
NotI (28)
BglII (35)
PmeI (44)
BGHpolyA
DraIII (300)
AscI (304)
KanaR
pMaxVax10.1
3710 bp
CMV Towne
NgoMI (1286)
NheI (1292)
BsrGI (2114)
EcoRV (2110)
ColE1 ori

Fig. 21

Fig. 22A

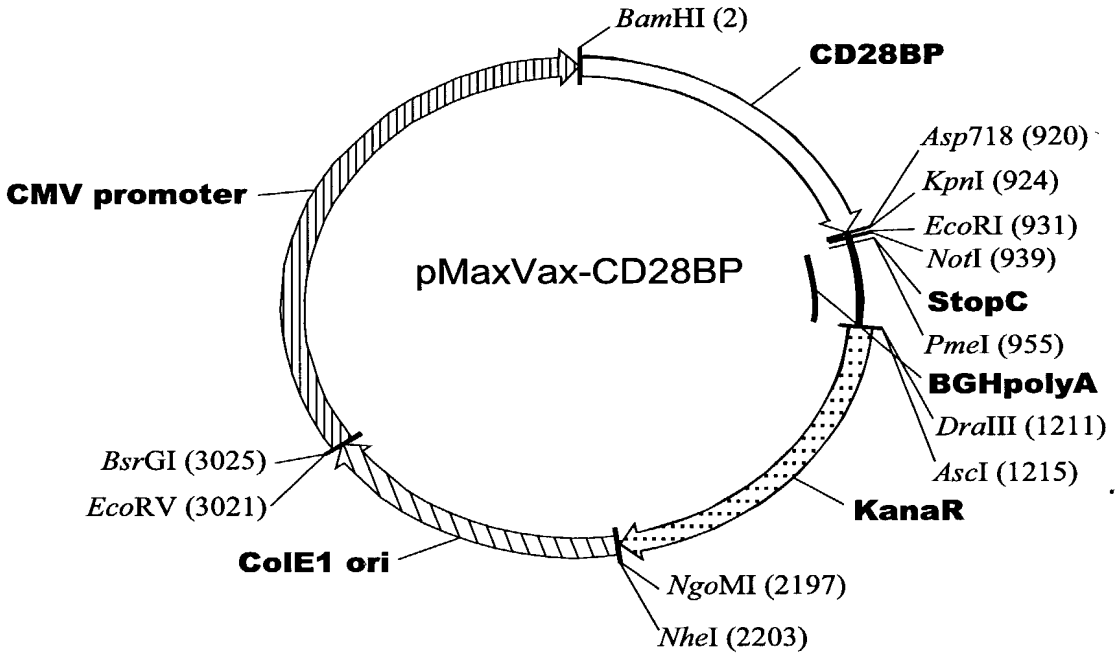


Fig. 22B